



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 130245**

**TO: Jeffrey Parkin**  
**Location: REM-3D39/3E18**  
**Art Unit: 1648**  
**Thursday, September 02, 2004**

**Case Serial Number: 10/001407**

**From: Toby Port**  
**Location: Biotech-Chem Library**  
**Remsen 1A59**  
**Phone: 571-272-2523**

**toby.port@uspto.gov**

### **Search Notes**

Dear Examiner Parkin,

Here are the results of your search.  
Please feel free to contact me if you have any questions.

Toby Port

U.S. FINE BLANK CORP.

From: Parkin, Jeffrey  
Sent: Wednesday, August 18, 2004 10:16 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence Search: U.S. Serial No. 10/001,407

Please search **SEQ ID NOS.: 10 and 15** from **U.S. Serial No. 10/001,407** (Yang, Y., and T. Burrell) v. all relevant databases, including interference. SEQ ID NO.: 10 corresponds to a region of the HIV-2 genome so it will probably pick up a large number of full-length sequences. **Can you limit the search results to pick up ONLY nucleic acid sequences that are =<100 nucleotides in length for both sequences?**

Place results on both disk and paper.

Thanks!

JSP  
REM 3D39  
AU 1648  
2-0908

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence :# \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 00:20:52 ; Search time 526.623 Seconds

(without alignments)  
2057.592 Million cell updates/sec

Title: US-10-001-407-10

Perfect score: 25

Sequence: 1 cggggcgcaaccctcctagggatttc 25

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 1846492

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

```
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ov:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rod:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	AX498422 Sequence
2	25	100.0	34	6	AX498420 Sequence
3	25	100.0	34	6	AX498421 Sequence
4	25	100.0	52	6	AX498427 Sequence
5	19	76.0	88	14	HIVLTRAAJ
6	18	72.0	25	6	AX498426 Sequence
7	18	72.0	58	6	AX498431
8	17	68.0	22	6	AR093423
9	17	68.0	22	6	E30948
10	16.6	66.4	24	6	AX498425 Sequence
11	16.6	66.4	32	6	BD161898
12	16.6	66.4	42	6	AR011291
13	16.6	66.4	42	6	I17929
14	16.6	66.4	57	6	AX498430
15	16.2	64.8	100	6	AX112460
16	16.2	64.8	100	6	AX112461
17	16	64.0	90	14	HIVTRAA
18	16	64.0	90	14	HIVTRAB
19	16	64.0	90	14	HIVTRAC
20	16	64.0	90	14	HIVTRAD
21	16	64.0	90	14	HIVTRAE
22	16	64.0	90	14	HIVTRAF
23	16	64.0	90	14	HIVTRAG
24	16	64.0	90	14	HIVTRAH
25	15.4	61.6	33	6	AR410466
26	15.4	61.6	33	6	AX317289
27	15.4	61.6	37	6	BD268930
28	15.4	61.6	37	6	AR302583
29	15.4	61.6	37	6	AX019151
30	15.4	61.6	37	6	AX035482
31	15.4	61.6	37	6	AX056855
32	15.4	61.6	37	6	BD130487
33	15.2	60.8	95	6	AX119975
34	15.2	60.8	95	6	AX138024
35	15	60.0	81	14	AF040785
36	15	60.0	81	14	AF040804
37	15	60.0	81	14	AF040854
38	15	60.0	89	14	HIVLTRAAI
39	15	60.0	89	14	HIVLTRAAJ
40	14.8	59.2	20	6	AX119964
41	14.8	59.2	20	6	AX138017
42	14.4	57.6	50	9	AY102626
43	14.4	57.6	52	6	AX347672
44	14.4	57.6	70	6	E33310
45	14.4	57.6	99	14	S63302

## ALIGNMENTS

RESULT 1  
AX498422 25 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 10 from Patent WO0234951.  
ACCESSION AX498422  
VERSION AX498422.1 GI:23343300  
KEYWORDS  
SOURCE Human immunodeficiency virus 2 (HIV-2)  
ORGANISM Human immunodeficiency virus 2  
Viruses; Retroviral; Retroviridae; Lentivirus; Primate  
Lentivirus group.  
REFERENCE  
AUTHORS Yang Y.Y. and Burrell T.A.  
TITLE Compositions and methods for detecting human immunodeficiency virus  
2 (hiv-2)

JOURNAL Patent: WO 0234951-A 10 02-MAY-2002;  
 FEATURES Gen-Probe Incorporated (US)  
 source Location/Qualifiers  
 1.25  
 /organism="Human immunodeficiency virus 2"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:11709"

Query Match 100.0%; Score 25; DB 6; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.87;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGGCGCAACCTGCTAGGATTTT 25  
 |||||  
 1 CGGGGCGCAACCTGCTAGGATTTT 25

RESULT 2  
 AX498420/c 34 bp DNA linear PAT 26-SEP-2002  
 LOCUS Sequence 8 from Patent WO0234951.  
 DEFINITION AX498420  
 ACCESSION AX498420  
 VERSION AX498420.1 GI:23343298  
 KEYWORDS  
 SOURCE Human immunodeficiency virus 2 (HIV-2)  
 ORGANISM  
 HUMAN immunodeficiency virus 2  
 Viruses; Retroviral viruses; Retroviridae; Lentivirus; Primate  
 lentivirus group.

REFERENCE  
 AUTHORS Yang, Y.Y. and Burrell, T.A.  
 TITLE Compositions and methods for detecting human immunodeficiency virus  
 2 (hiv-2)  
 JOURNAL Patent: WO 0234951-A 8 02-MAY-2002;  
 FEATURES Gen-Probe Incorporated (US)  
 source Location/Qualifiers  
 1.34  
 /organism="Human immunodeficiency virus 2"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:11709"

ORIGIN  
 Query Match 100.0%; Score 25; DB 6; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 0.84;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGGCGCAACCTGCTAGGATTTT 25  
 |||||  
 25 CGGGGCGCAACCTGCTAGGATTTT 1

RESULT 3  
 AX498421 34 bp DNA linear PAT 26-SEP-2002  
 LOCUS Sequence 9 from Patent WO0234951.  
 DEFINITION AX498421  
 ACCESSION AX498421  
 VERSION AX498421.1 GI:23343299  
 KEYWORDS  
 SOURCE Human immunodeficiency virus 2 (HIV-2)  
 ORGANISM  
 HUMAN immunodeficiency virus 2  
 Viruses; Retroviral viruses; Retroviridae; Lentivirus; Primate  
 lentivirus group.  
 REFERENCE  
 AUTHORS Yang, Y.Y. and Burrell, T.A.  
 TITLE Compositions and methods for detecting human immunodeficiency virus  
 2 (hiv-2)  
 JOURNAL Patent: WO 0234951-A 9 02-MAY-2002;  
 FEATURES Gen-Probe Incorporated (US)  
 source Location/Qualifiers  
 1.34  
 /organism="Human immunodeficiency virus 2"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:11709"

## ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 0.84;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGGCGCAACCTGCTAGGATTTT 25  
 |||||  
 10 CGGGGCGCAACCTGCTAGGATTTT 34

RESULT 4  
 AX498427 52 bp DNA linear PAT 26-SEP-2002  
 LOCUS Sequence 15 from Patent WO0234951.  
 DEFINITION AX498427  
 ACCESSION AX498427  
 VERSION AX498427.1 GI:23343305  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM  
 synthetic construct  
 artificial sequences.

REFERENCE  
 AUTHORS Yang, Y.Y. and Burrell, T.A.  
 TITLE Compositions and methods for detecting human immunodeficiency virus  
 2 (hiv-2)  
 JOURNAL Patent: WO 0234951-A 15 02-MAY-2002;  
 FEATURES Gen-Probe Incorporated (US)  
 source Location/Qualifiers  
 1.52  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="T7 promoter primer having a promoter sequence  
 appended at the 5' end of an HIV-2 complementary primer  
 sequence"

ORIGIN  
 Query Match 100.0%; Score 25; DB 6; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 0.8;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGGCGCAACCTGCTAGGATTTT 25  
 |||||  
 28 CGGGGCGCAACCTGCTAGGATTTT 52

RESULT 5  
 HIVTRAJ/c 88 bp DNA linear VRL 02-AUG-1993  
 LOCUS partial sequence, clone 1.  
 DEFINITION Human immunodeficiency virus type 2 long terminal repeat region,  
 M74763  
 ACCESSION M74763.1 GI:327981  
 VERSION long terminal repeat (LTR).  
 KEYWORDS Human immunodeficiency virus 2 (HIV-2)  
 SOURCE Human immunodeficiency virus 2  
 ORGANISM  
 HUMAN immunodeficiency virus 2  
 Viruses; Retroviral viruses; Retroviridae; Lentivirus; Primate  
 lentivirus group.  
 REFERENCE  
 AUTHORS Whitcomb, J.M. and Hughes, S.H.  
 TITLE The sequence of human immunodeficiency virus type 2 circle junction  
 suggests that integration protein cleaves the ends of linear DNA  
 asymmetrically  
 JOURNAL J. Virol. 65 (7), 3906-3910 (1991)  
 MEDLINE 91251249  
 PUBMED 2041100  
 COMMENT Original source text: Human immunodeficiency virus type 2 DNA.  
 FEATURES  
 source Location/Qualifiers  
 1.88  
 /organism="Human immunodeficiency virus 2"  
 /proviral  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:11709"

LTR 1. .88

ORIGIN

Query Match 76.0%; Score 19; DB 14; Length 88;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCAACCTGCTAGGATTTT 25  
DB 48 CCAACCTGCTAGGATTTT 30

RESULT 6  
AX498426  
LOCUS AX498426 25 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 14 from Patent WO0234951.  
ACCESSION AX498426  
VERSION AX498426.1 GI:23343304  
KEYWORDS  
SOURCE Human immunodeficiency virus 2 (HIV-2)  
ORGANISM Human immunodeficiency virus 2 (HIV-2)  
VIRUSES; Retroviridae; Lentivirus; Primate  
Lentivirus group.

REFERENCE  
AUTHORS Yang, Y.Y. and Burrell, T.A.  
TITLE Compositions and methods for detecting human immunodeficiency virus  
JOURNAL Patent: WO 0234951-A 14 02-MAY-2002;  
Gen-Probe Incorporated (US)  
FEATURES  
source 1. .25  
/organism="Human immunodeficiency virus 2"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:11709"

ORIGIN

Query Match 72.0%; Score 18; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCGCCCAACTGCTAG 18  
DB 8 CGGGCGCCCAACTGCTAG 25

RESULT 7  
AX498431  
LOCUS AX498431 58 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 19 from Patent WO0234951.  
ACCESSION AX498431  
VERSION AX498431.1 GI:23343309  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE  
AUTHORS Yang, Y.Y. and Burrell, T.A.  
TITLE Compositions and methods for detecting human immunodeficiency virus  
JOURNAL Patent: WO 0234951-A 19 02-MAY-2002;  
Gen-Probe Incorporated (US)  
FEATURES  
source 1. .58  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="T7 promoter primer having a promoter sequence  
appended at the 5' end of an HIV-2 complementary primer  
sequence"

ORIGIN

Query Match 72.0%; Score 18; DB 6; Length 58;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCGCCCAACTGCTAG 18  
DB 41 CGGGCGCCCAACTGCTAG 58

RESULT 8  
AR093423  
LOCUS AR093423 22 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 31 from patent US 6001558.  
ACCESSION AR093423  
VERSION AR093423.1 GI:10020172  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE  
AUTHORS Backus, J.W., Atwood, S.M., Casey, A.E., Rasmussen, E.B. and  
Cummins, T.J.  
TITLE Amplification and detection of HIV-1 and/or HIV 2  
JOURNAL Patent: US 6001558-A 31 14-DEC-1999;  
Gen-Probe Incorporated (US)  
FEATURES  
source 1. .22  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 68.0%; Score 17; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCGCCCAACTGCTA 17  
DB 6 CGGGCGCCCAACTGCTA 22

RESULT 9  
E30948  
LOCUS E30948 22 bp DNA linear PAT 18-JUN-2001  
DEFINITION Amplification and detection of HIV-1 and/or HIV-2.  
ACCESSION E30948  
VERSION E30948.1 GI:13025679  
KEYWORDS JP 1999069987-A/31.  
SOURCE unidentified  
ORGANISM unidentified  
Unclassified.

REFERENCE  
AUTHORS John, W.B., Suzan, M.A., Ann, E.K., Eric, B.R. and Thomas, J.K.  
TITLE Amplification and detection of HIV-1 and/or HIV-2  
JOURNAL Patent: JP 1999069987-A 31 16-MAR-1999;  
ORTHO CLINICAL DIAGNOSTICS INC  
COMMENT OS Unidentified  
PN JP 1999069987-A/31  
PD 16-MAR-1999  
PF 24-JUN-1998 JP 1998177059  
PR 25-JUN-1997 US 60/050759  
PI JOHN WESLEY BACKUS, SUZAN MERISSA ATTWOOD, ANN ELIZABETH KEIJI,  
ERIC BRICE RASMUSSEN, THOMAS JOSEPH KAMINZU  
PC C12N15/09, C1201/68, G01N33/566, G01N33/569, C12N15/00 CC  
Strandness: Single;  
CC Topology: linear;  
FH Key  
FT source 1. .22  
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Location/Qualifiers  
location/Qualifiers  
1. .22  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 68.0%; Score 17; DB 6; Length 22;

Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGCCACCTGCTAGGATTT 17  
DB 6 CGGCGCCACCTGCTAGGATTT 22

## RESULT 10

AX498425

LOCUS

AX498425 Sequence 13 from Patent WO0234951. 24 bp DNA linear PAT 26-SEP-2002  
AX498425 ACCESSION  
AX498425.1 GI:23343303 VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
Source

1  
synthetic construct  
artificial sequences.

Yang, Y. Y. and Burrell, T. A.  
Compositions and methods for detecting human immunodeficiency virus  
2 (hiv-2)  
Patent: WO 0234951-A 13 02-MAY-2002;  
Gen-Probe Incorporated (US)  
Location/Qualifiers  
1. .24

/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer mismatches HIV-2 sequence by deletion of one nucleotide"

## ORIGIN

Query Match 66.4%; Score 16.6; DB 6; Length 24;  
Best Local Similarity 82.6%; Pred. No. 1e+04;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGGCGCCACCTGCTAGGATTTT 25  
DB 2 GGGCGCCACCTGCTAGGATTTT 24

RESULT 11  
BD161898  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

BD161898 Nonhuman primate model of acquired immunodeficiency syndrome.  
BD161898  
BD161898.1 GI:27867656  
UP 2002159296-A/7.  
synthetic construct  
artificial sequences.  
1 (bases 1 to 32)  
Nonhuman primate model of acquired immunodeficiency syndrome  
Patent: JP 2002159296-A 7 04-JUN-2002;  
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIOUS DISEASES, THE  
ORGANIZATION FOR PHARMACEUTICAL SAFETY AND RESEARCH  
OS  
JP 2002159296-A/7  
PD 27-NOV-2000 JP 200360274  
PI KATSUAKI SHINOHARA, KOJI SAKAI, MITSUO HONDA  
PC C12N15/09, A01K67/027, C12N7/00, C12N7/02, G01N33/15, G01N33/50//  
PC G01N33/569,  
PC (C12N7/00, C12R1:93), (C12N7/02, C12R1:93), C12N15/00 CC  
Description of Artificial Sequence: artificially synthesized CC  
primer  
CC  
sequence  
FH Key  
FT source  
Location/Qualifiers  
1. .32  
/organism="Artificial Sequence".  
Location/Qualifiers

## Source

1. .32  
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/db\_xref="taxon:32630"

Query Match 66.4%; Score 16.6; DB 6; Length 32;  
Best Local Similarity 82.6%; Pred. No. 9.7e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGGCGCCACCTGCTAGGATTTT 25  
DB 1 GGGCGATTTCTGCTAGGATTTT 23

## RESULT 12

AR011291

LOCUS

AR011291 Sequence 160 from patent US 5762938. 42 bp DNA linear PAT 04-DEC-1998  
AR011291 ACCESSION  
AR011291.1 GI:3969281 VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
Source

1  
Unclassified.  
1 (bases 1 to 42)  
Paoletti, E., Perkus, M. E., Taylor, J., Tartaglia, J., Norton, B. K.,  
Riviere, M., de Taisne, C., Limbach, K. J., Johnson, G. P., Pincus, S. E.,  
Cox, W. I., Audonnet, J.-C., Francis, and Gettig, R. Robert.  
Modified recombinant vaccinia virus and expression vectors thereof  
Patent: US 5762938-A 160 09-JUN-1998;  
Location/Qualifiers  
1. .42

## ORIGIN

Query Match 66.4%; Score 16.6; DB 6; Length 42;  
Best Local Similarity 82.6%; Pred. No. 9.4e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGCGCCACCTGCTAGGATTT 24  
DB 9 GGGCATCAGACCTAGGATTT 31

RESULT 13  
117929  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
Source

117929 Sequence 160 from patent US 5494807. 42 bp DNA linear PAT 07-OCT-1996  
117929  
117929.1 GI:1598284  
Unclassified.  
1 (bases 1 to 42)  
Paoletti, E., Perkus, M. E., Taylor, J., Tartaglia, J., Norton, B. K.,  
Riviere, M., de Taisne, C., Limbach, K. J., Johnson, G. P., Pincus, S. E.,  
Cox, W. I., Audonnet, J.-C., Francis, and Gettig, R. R.  
NYVAC vaccine virus recombinants comprising heterologous inserts  
Patent: US 5494807-A 160 27-FEB-1996;  
Location/Qualifiers  
1. .42  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Query Match 66.4%; Score 16.6; DB 6; Length 42;  
Best Local Similarity 82.6%; Pred. No. 9.4e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGCGCCACCTGCTAGGATTT 24

Db 9 GGGCATCAAGACGCTAGGATTT 31

Search completed: August 31, 2004, 02:04:24  
job time : 527.623 secs

RESULT 14  
LOCUS AX498430 57 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 18 from Patent WO0234951.  
ACCESSION AX498430  
VERSION AX498430.1 GI:23343308  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Yang, Y.Y. and Burrell, T.A.  
TITLE Compositions and methods for detecting human immunodeficiency virus  
2 (hiv-2)  
JOURNAL Patent: WO 0234951-A 18 02-MAY-2002;  
Gen-Probe Incorporated (US)  
FEATURES  
Location/Qualifiers  
1..57  
source  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="T7 promoter primer having a promoter sequence  
appended at the 5' end of the sequence given as SEQ ID  
NO:13"

## ORIGIN

Query Match 66.4%; Score 16.6; DB 6; Length 57;  
Best Local Similarity 82.6%; Pred. No. 9.1e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGGCGCACTGCTAGGATTTT 25  
Db 35 GGGCGCACTGCTAGGATTTT 57

RESULT 15  
LOCUS AX112460 100 bp DNA linear PAT 01-MAY-2001  
DEFINITION Sequence 108 from Patent WO0127857.  
ACCESSION AX112460  
VERSION AX112460.1 GI:13939219  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Braun, A., Koester, H., van den Boom, D., Ping, Y., Rodl, C., He, L.,  
Chiu, N. and Jurinke, C.  
TITLE Methods for generating databases and databases for identifying  
polymorphic genetic markers  
JOURNAL Patent: WO 0127857-A 108 19-APR-2001;  
Sequenom, Inc. (US)  
FEATURES  
source  
1..100  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 64.8%; Score 16.2; DB 6; Length 100;  
Best Local Similarity 85.7%; Pred. No. 1.3e+04;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGCGCACTGCTAGGAT 22  
Db 64 GGGCGCACTGCTAGGAT 84

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model.

Run on: August 31, 2004, 00:19:57 ; Search time 164.935 Seconds  
(without alignments)  
643.920 Million cell updates/sec

Title: US-10-001-407-10

Perfect score: 25

Sequence: 1 cggcgcccaaccctcctaggatctt 25

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 337863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 3485926

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1980s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	6	ABK93886 Human imm
2	25	100.0	34	6	ABK93885 Human imm
3	25	100.0	34	6	ABK93884 Human imm
4	25	100.0	52	6	ABK93891 Human imm
5	18	72.0	25	6	ABK93890 Human imm
6	18	72.0	58	6	ABK93895 Human imm
7	17	68.0	22	2	AAV63697 PCR prime
8	16.6	66.4	24	6	ABK93889 Human imm
9	16.6	66.4	42	2	AAQ35348 Human imm
10	16.6	66.4	57	6	ABK93894 Human imm
11	16.2	64.8	100	4	AAH02411 Human Pac
12	16.2	64.8	100	4	AAH02412 Human Pac
13	15.8	63.2	33	7	ACC00078 Primer #4
14	15.6	62.4	41	6	ABA05816 Human ubi
15	15.4	61.6	33	2	AAT68636 VI/T2 sub
16	15.4	61.6	33	2	AAZ21588 Oligonuc
17	15.4	61.6	33	2	AAZ02151 Mouse REN
18	15.4	61.6	37	2	AAZ08739 HCMV/HIV
19	15.4	61.6	37	3	AAU94001 Antiviral
20	15.4	61.6	37	4	AAAC86895 PCR prime
21	15.2	60.8	95	6	ABK11007 Oligonuc
22	14.8	59.2	20	6	ABK11001 TTV-apopt
23	14.4	57.6	52	6	ABX09698 G. rostris

24	14.4	57.6	65	7	ACC69414 Chicken c
25	14.4	57.6	65	8	ACC69376 Chicken c
26	14.4	57.6	70	3	AAAI2580 Synthetic
27	14.4	57.6	90	9	ADBB7801 gp120 sig
28	14.4	57.6	90	9	ADDB66325 HIV gp120
29	14.2	56.8	51	4	AAH37460 Human SNP
30	14.2	56.8	67	6	ABK44261 Complement
31	14.2	56.8	67	6	ABK67491 DNA encod
32	14.2	56.8	67	9	ADE11051 Chimeric
33	14.2	56.8	75	6	ABK44260 DNA encod
34	14.2	56.8	75	6	ABK67490 DNA encod
35	14.2	56.8	75	9	ADE11050 Chimeric
36	14.2	56.8	82	4	ABA74362 Human foe
37	14.2	56.8	82	4	AAI54827 Probe #23
38	14.2	56.8	82	4	AAK48999 Human bon
39	14.2	56.8	82	4	AAK22828 Human bra
40	14.2	56.8	82	4	ABS48660 Human liv
41	14.2	56.8	82	6	ABS22635 Human gen
42	14	56.0	41	2	AAV50944 Maize pol
43	14	56.0	41	6	ABA05815 Human ubi
44	14	56.0	50	4	AAI31122 Human SNP
45	14	56.0	65	6	ABK16412 Asbnya go

## ALIGNMENTS

RESULT 1  
ABK93886 standard; DNA; 25 BP.

XX  
AC ABK93886;  
XX  
AC 29-AUG-2003 (revised)  
DT 26-AUG-2002 (first entry)  
XX  
DE Human immunodeficiency virus type 2 detection probe #10.  
XX  
KW Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;  
KW hepatitis C virus; HCV; probe; ss.  
XX  
OS Human immunodeficiency virus 2.  
XX  
PN W0200234951-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 22-OCT-2001; 2001WO-US045396.  
XX  
PR 23-OCT-2000; 2000US-0242620P.  
PR 30-MAR-2001; 2001US-0280058P.  
PA (GENP-) GEN-PROBE INC.  
PI Yang Y, Burrell TA;  
PI WPI; 2002-489953/52.  
XX  
DR  
XX  
PT Detecting human immunodeficiency virus-2 nucleic acids in a sample, by  
PT amplifying nucleic acids with oligonucleotides and detecting nucleic  
PT acid, or hybridizing nucleic acid with a probe and detecting probe:target  
PT duplex.  
XX  
PS Claim 10; Page 25; 58pp; English.  
XX  
CC The invention relates to a method of detecting human immunodeficiency  
CC virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with  
CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide  
CC base sequence, and detecting the amplified NA; or providing a  
CC hybridisation probe and detectable label, hybridising HIV-2 NA with the  
CC probe to form probe:target duplex, and detecting the duplex. The method  
CC is useful for detecting the presence of HIV-2 NAs in a lysate or a blood  
CC product such as plasma or serum, and also for detecting subtypes A, B, C

CC and D of HIV-2. The method is useful for amplifying and detecting the NA  
CC in blood serum and also as components of multiplex amplification  
CC reactions that synthesize amplicons corresponding to polynucleotides of  
CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C  
CC virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the  
CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX  
SQ Sequence 25 BP; 4 A; 7 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCGCCCACTGCTAGGATTTT 25  
Db 1 CGGGCGCCCACTGCTAGGATTTT 25

RESULT 2  
ABK93885  
ID ABK93885 standard; DNA; 34 BP.

XX  
AC ABK93885;

XX  
DT 29-AUG-2003 (revised)

XX  
DT 26-AUG-2002 (first entry)

XX  
DE Human immunodeficiency virus type 2 detection probe #9.

XX  
KW Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;  
XX hepatitis C virus; HCV; probe; ss.

XX  
OS Human immunodeficiency virus 2.

XX  
PN WO200234951-A2.

XX  
PD 02-MAY-2002.

XX  
PF 22-OCT-2001; 2001WO-US045396.

XX  
PR 23-OCT-2000; 2000US-0242620P.  
XX 30-MAR-2001; 2001US-0280058P.

XX  
PA (GENP-) GEN-PROBE INC.

XX  
PI Yang YF, Burrell TA;

XX  
DR WPI; 2002-489953/52.

XX  
PT Detecting human immunodeficiency virus-2 nucleic acids in a sample, by  
XX amplifying nucleic acids with oligonucleotides and detecting nucleic  
XX acid, or hybridizing nucleic acid with a probe and detecting probe:target  
XX duplex.

XX  
PS Claim 1; Page 22; 58pp; English.

XX  
CC The invention relates to a method of detecting human immunodeficiency  
CC virus-2 nucleic acids (NA) in a biological sample, by contacting NA with  
CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide  
CC base sequence, and detecting the amplified NA; or providing a  
CC hybridisation probe and detecting the amplified NA; or providing a  
CC probe to form probe:target duplex, and detecting the duplex. The method  
CC is useful for detecting the presence of HIV-2 NA in a lysate or a blood  
CC product such as plasma or serum, and also for detecting subtypes A, B, C  
CC and D of HIV-2. The method is useful for amplifying and detecting the NA  
CC in blood serum and also as components of multiplex amplification  
CC reactions that synthesize amplicons corresponding to polynucleotides of  
CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C  
CC virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the  
CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX  
SQ Sequence 34 BP; 4 A; 10 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCGCCCACTGCTAGGATTTT 25  
Db 10 CGGGCGCCCACTGCTAGGATTTT 34

RESULT 3  
ABK93884/C  
ID ABK93884 standard; DNA; 34 BP.

XX  
AC ABK93884;

XX  
DT 29-AUG-2003 (revised)

XX  
DT 26-AUG-2002 (first entry)

XX  
DE Human immunodeficiency virus type 2 detection probe #8.

XX  
KW Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;  
XX hepatitis C virus; HCV; probe; ss.

XX  
OS Human immunodeficiency virus 2.

XX  
PN WO200234951-A2.

XX  
PD 02-MAY-2002.

XX  
PF 22-OCT-2001; 2001WO-US045396.

XX  
PR 23-OCT-2000; 2000US-0242620P.  
XX 30-MAR-2001; 2001US-0280058P.

XX  
PA (GENP-) GEN-PROBE INC.

XX  
PI Yang YF, Burrell TA;

XX  
DR WPI; 2002-489953/52.

XX  
PT Detecting human immunodeficiency virus-2 nucleic acids in a sample, by  
XX amplifying nucleic acids with oligonucleotides and detecting nucleic  
XX acid, or hybridizing nucleic acid with a probe and detecting probe:target  
XX duplex.

XX  
PS Example 1; Page 39; 58pp; English.

XX  
CC The invention relates to a method of detecting human immunodeficiency  
CC virus-2 nucleic acids (NA) in a biological sample, by contacting NA with  
CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide  
CC base sequence, and detecting the amplified NA; or providing a  
CC hybridisation probe and detecting the amplified NA; or providing a  
CC probe to form probe:target duplex, and detecting the duplex. The method  
CC is useful for detecting the presence of HIV-2 NA in a lysate or a blood  
CC product such as plasma or serum, and also for detecting subtypes A, B, C  
CC and D of HIV-2. The method is useful for amplifying and detecting the NA  
CC in blood serum and also as components of multiplex amplification  
CC reactions that synthesize amplicons corresponding to polynucleotides of  
CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C  
CC virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the  
CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX  
SQ Sequence 34 BP; 10 A; 10 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCGCCCACTGCTAGGATTTT 25  
Db 25 CGGGCGCCCACTGCTAGGATTTT 1



```
RESULT 4
ABK93891
ID ABK93891 standard; DNA; 52 BP.
AC ABK93891;
XX
XX
XX 29-AUG-2003 (revised)
DT 26-AUG-2002 (first entry)
XX
XX Human immunodeficiency virus type 2 detection probe #15.
DE
XX Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;
KM hepatitis C virus; HCV; probe; ss.
XX
XX Human immunodeficiency virus 2.
OS
XX WO200234951-A2.
PN
XX 02-MAY-2002.
PD
XX 22-OCT-2001; 2001WO-US045396.
PF
XX 23-OCT-2000; 2000US-0242620P.
PR 30-MAR-2001; 2001US-0280058P.
XX
XX (GENP-) GEN-PROBE INC.
PA
XX Yang YY, Burrell TA;
PI
XX WPI; 2002-489953/52.
XX
XX Detecting human immunodeficiency virus-2 nucleic acids in a sample, by
PT amplifying nucleic acids with oligonucleotides and detecting nucleic
PT acid, or hybridizing nucleic acid with a probe and detecting probe:target
XX duplex.
XX
XX Claim 11; Page 25; 58pp; English.
XX
XX The invention relates to a method of detecting human immunodeficiency
CC virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with
CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide
CC base sequence, and detecting the amplified NA; or providing a
CC hybridisation probe and detectable label, hybridising HIV-2 NA with the
CC probe to form probe:target duplex, and detecting the duplex. The method
CC is useful for detecting the presence of HIV-2 NAs in a lysate or a blood
CC product such as plasma or serum, and also for detecting subtypes A, B, C
CC and D of HIV-2. The method is useful for amplifying and detecting the NA
CC in blood serum and also as components of multiplex amplification
CC reactions that synthesise amplicons corresponding to polynucleotides of
CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C
CC virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX
XX Sequence 52 BP; 15 A; 11 C; 13 G; 13 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 25; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCGCCCAACTGCTAGGATTTT 25
Db 28 CGGGCGCCCAACTGCTAGGATTTT 52
```

```
DE Human immunodeficiency virus type 2 detection probe #14.
XX
XX Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;
KM hepatitis C virus; HCV; probe; ss.
XX
XX Human immunodeficiency virus 2.
OS
XX WO200234951-A2.
PN
XX 02-MAY-2002.
PD
XX 22-OCT-2001; 2001WO-US045396.
PF
XX 23-OCT-2000; 2000US-0242620P.
PR 30-MAR-2001; 2001US-0280058P.
XX
XX (GENP-) GEN-PROBE INC.
PA
XX Yang YY, Burrell TA;
PI
XX WPI; 2002-489953/52.
XX
XX Detecting human immunodeficiency virus-2 nucleic acids in a sample, by
PT amplifying nucleic acids with oligonucleotides and detecting nucleic
PT acid, or hybridizing nucleic acid with a probe and detecting probe:target
XX duplex.
XX
XX Claim 10; Page 25; 58pp; English.
XX
XX The invention relates to a method of detecting human immunodeficiency
CC virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with
CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide
CC base sequence, and detecting the amplified NA; or providing a
CC hybridisation probe and detectable label, hybridising HIV-2 NA with the
CC probe to form probe:target duplex, and detecting the duplex. The method
CC is useful for detecting the presence of HIV-2 NAs in a lysate or a blood
CC product such as plasma or serum, and also for detecting subtypes A, B, C
CC and D of HIV-2. The method is useful for amplifying and detecting the NA
CC in blood serum and also as components of multiplex amplification
CC reactions that synthesise amplicons corresponding to polynucleotides of
CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C
CC virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX
XX Sequence 25 BP; 3 A; 10 C; 7 G; 5 T; 0 U; 0 Other;
SQ
Query Match 72.0%; Score 18; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCGCCCAACTGCTAG 18
Db 8 CGGGCGCCCAACTGCTAG 25
```

```
RESULT 6
ABK93895
ID ABK93895 standard; DNA; 58 BP.
AC ABK93895;
XX
XX
XX 29-AUG-2003 (revised)
DT 26-AUG-2002 (first entry)
XX
XX Human immunodeficiency virus type 2 detection probe #19.
DE
XX Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;
KM hepatitis C virus; HCV; probe; ss.
XX
XX Human immunodeficiency virus 2.
OS
XX WO200234951-A2.
XX
```

PD 02-MAY-2002.

XX 22-OCT-2001; 2001MO-US045396.

XX 23-OCT-2000; 2000US-0242620P.

XX 30-MAR-2001; 2001US-0280058P.

XX (GENP-) GEN-PROBE INC.

XX Yang YY, Burrell TA;

XX WPI; 2002-489953/52.

XX Detecting human immunodeficiency virus-2 nucleic acids in a sample, by  
XX amplifying nucleic acids with oligonucleotides and detecting nucleic  
XX acid, or hybridizing nucleic acid with a probe and detecting probe:target  
XX duplex.

XX Claim 11; Page 25; 58pp; English.

XX The invention relates to a method of detecting human immunodeficiency  
XX virus-2 nucleic acids (NA) in a biological sample, by contacting NA with  
XX 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleic acid  
XX base sequence, and detecting the amplified NA; or providing a  
XX hybridization probe and detecting the amplified NA; or providing a  
XX probe to form probe:target duplex, and detecting the duplex. The method  
XX is useful for detecting the presence of HIV-2 NA in a lysate or a blood  
XX product such as plasma or serum, and also for detecting subtypes A, B, C  
XX and D of HIV-2. The method is useful for amplifying and detecting the NA  
XX in blood serum and also as components of multiplex amplification  
XX reactions that synthesize amplicons corresponding to polynucleotides of  
XX unrelated viruses, e.g., HIV-1, hepatitis B virus (HBV) and hepatitis C  
XX virus (HCV). ABR93877-ABK93910 represent HIV-2 detection probes of the  
XX invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 58 BP; 17 A; 17 C; 13 G; 11 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 72.0%; Score 18; DB 6; Length 58;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCGCCAACTGCTAG 18  
DB 41 CGGGCGCCAACTGCTAG 58

XX RESULT 7

XX ID AAV63697 standard; DNA; 22 BP.

XX AC AAV63697;

XX 11-MAR-1999 (first entry)

XX PCR primer used to amplify HIV-2 sequences.

XX HIV-1; HIV-2; detection; Acquired Immunodeficiency Syndrome; AIDS;  
XX co-amplification assay; PCR primer; ss.

XX Synthetic.

XX Human immunodeficiency virus 2.

XX EP887427-A2.

XX 30-DEC-1998.

XX 24-JUN-1998; 98EP-00304959.

XX 25-JUN-1997; 97US-0050759P.

XX (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.

XX Beckus JW, Atwood SM, Casey AE, Rasmussen EB, Cummins TJ;

XX WPI; 1999-047891/05.

XX Detecting Human Immunodeficiency Virus 1 and 2 - using at least four new  
XX oligonucleotide primers and multiple detection probes.

XX Disclosure; Page 11; 25pp; English.

XX The present PCR primer is used to amplify human deficiency type 2 (HIV-2)  
XX nucleic acids. The specification also describes primers and probes for  
XX HIV-1 and HIV-2. The primers and probes are useful for amplifying and  
XX detecting HIV-1 and HIV-2 and all their subtype nucleic acids in  
XX biological samples; and for giving progress in our understanding of  
XX Acquired Immunodeficiency Syndrome (AIDS). The primers are able to detect  
XX all HIV-1 and HIV-2 subtypes without detecting non-related viruses. The  
XX primer sets for HIV-1 and HIV-2 are compatible with each other, and can  
XX be combined to form a co-amplification assay for HIV-1 and HIV-2. Using  
XX more than one primer set to amplify target nucleic acid sequences which  
XX overlap a common probe region maximises strain sensitivity and robustness

XX Sequence 22 BP; 3 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 68.0%; Score 17; DB 2; Length 22;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCGCCAACTGCTA 17  
DB 6 CGGGCGCCAACTGCTA 22

XX RESULT 8

XX ID ABR93889 standard; DNA; 24 BP.

XX AC ABR93889;

XX 29-AUG-2003 (revised)

XX 26-AUG-2002 (first entry)

XX Human immunodeficiency virus type 2 detection probe #13.

XX Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;  
XX hepatitis C virus; HCV; probe; ss.

XX Human immunodeficiency virus 2.

XX WO200234951-A2.

XX 02-MAY-2002.

XX 22-OCT-2001; 2001MO-US045396.

XX 23-OCT-2000; 2000US-0242620P.

XX 30-MAR-2001; 2001US-0280058P.

XX (GENP-) GEN-PROBE INC.

XX Yang YY, Burrell TA;

XX WPI; 2002-489953/52.

XX Detecting human immunodeficiency virus-2 nucleic acids in a sample, by  
XX amplifying nucleic acids with oligonucleotides and detecting nucleic  
XX acid, or hybridizing nucleic acid with a probe and detecting probe:target  
XX duplex.

XX Claim 10; Page 25; 58pp; English.

XX The invention relates to a method of detecting human immunodeficiency  
XX virus-2 nucleic acids (NA) in a biological sample, by contacting NA with  
XX 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleic acid  
XX base sequence, and detecting the amplified NA; or providing a

CC hybridisation probe and detectable label, hybridising HIV-2 NA with the  
 CC probe to form probe:target duplex, and detecting the duplex. The method  
 CC is useful for detecting the presence of HIV-2 NAs in a lysate or a blood  
 CC product such as plasma or serum, and also for detecting subtypes A, B, C  
 CC and D of HIV-2. The method is useful for amplifying and detecting the NA  
 CC in blood serum and also as components of multiplex amplification  
 CC reactions that synthesise amplicons corresponding to polynucleotides of  
 CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C  
 CC virus (HCV). ABR93877-ABK93910 represent HIV-2 detection probes of the  
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 24 BP; 3 A; 7 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 66.4%; Score 16.6; DB 6; Length 24;  
 Best Local Similarity 82.6%; Pred. No. 1.8e+02;  
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGGCCCAACCTGCTAGGATTTT 25  
 |||  
 Db 2 GGGCCCAACCTGCTAGGATTTT 24

RESULT 9  
 ID AAO35348 standard; DNA; 42 BP.

XX AAO35348;

XX 25-MAR-2003 (revised)  
 DT 18-MAY-1993 (first entry)

XX MUENSIVIR, a mutagenesis primer for env gene.

XX Human immunodeficiency virus; HIV; amplification; ss.

XX Synthetic.

XX WO9222641-A1.

XX 23-DEC-1992.

XX 12-JUN-1992; 92WO-US005107.

XX 14-JUN-1991; 91US-00715921.

XX 11-JUN-1992; 92US-00897382.

XX (VIRO-) VIROGENETICS CORP.

XX Paolletti E, Tartaglia J, Cox WJ;

XX WPI; 1993-018128/02.

XX Modified recombinant virus with inactivated non-essential genetic  
 PT functions - comprises e.g. vaccinia or avipox virus, used as HIV vaccine.

XX Example 3; Page 49; 159pp; English.

XX The env gene of HIV was subjected to in vitro mutagenesis to remove the  
 CC sequences encoding the rex protein and the LTR region from the 3' end of  
 CC the gene and to delete the putative immuno-suppressive (IS) region (amino  
 CC acids 583-599). Mutagenesis was performed using primers LTR and  
 CC MUENSIVIR using PIR25mutenv8 as template. Mutagenised clones were  
 CC identified by hybridisation and restriction analysis. See also AAO35328-  
 CC 437. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 42 BP; 8 A; 8 C; 15 G; 11 T; 0 U; 0 Other;

Query Match 66.4%; Score 16.6; DB 2; Length 42;  
 Best Local Similarity 82.6%; Pred. No. 2e+02;  
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGCCCAACCTGCTAGGATTT 24  
 |||

Db 9 GGGCATCAGCAGCTAGGATTT 31

RESULT 10

ID ABR93894 standard; DNA; 57 BP.

XX ABR93894;

XX 29-AUG-2003 (revised)  
 DT 26-AUG-2002 (first entry)

XX Human immunodeficiency virus type 2 detection probe #18.

XX Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;

KM hepatitis C virus; HCV; probe; ss.

XX Human immunodeficiency virus 2.

XX WO200234951-A2.

XX 02-MAY-2002.

XX 22-OCT-2001; 2001WO-US045396.

XX 23-OCT-2000; 2000US-0242620P.

XX 30-MAR-2001; 2001US-0280058P.

XX (GENP-) GEN-PROBE INC.

XX Yang YY, Burrell TA;

XX WPI; 2002-489953/52.

XX Detecting human immunodeficiency virus-2 nucleic acids in a sample, by  
 PT amplifying nucleic acids with oligonucleotides and detecting nucleic  
 PT acid, or hybridizing nucleic acid with a probe and detecting probe:target  
 PT duplex.

XX Claim 11; Page 25; 58pp; English.

XX The invention relates to a method of detecting human immunodeficiency  
 CC virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with  
 CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide  
 CC base sequence, and detecting the amplified NA, or providing a  
 CC hybridisation probe and detectable label, hybridising HIV-2 NA with the  
 CC probe to form probe:target duplex, and detecting the duplex. The method  
 CC is useful for detecting the presence of HIV-2 NAs in a lysate or a blood  
 CC product such as plasma or serum, and also for detecting subtypes A, B, C  
 CC and D of HIV-2. The method is useful for amplifying and detecting the NA  
 CC in blood serum and also as components of multiplex amplification  
 CC reactions that synthesise amplicons corresponding to polynucleotides of  
 CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C  
 CC virus (HCV). ABR93877-ABK93910 represent HIV-2 detection probes of the  
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 57 BP; 17 A; 14 C; 14 G; 12 T; 0 U; 0 Other;

Query Match 66.4%; Score 16.6; DB 6; Length 57;  
 Best Local Similarity 82.6%; Pred. No. 2.1e+02;  
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGGCCCAACCTGCTAGGATTTT 25  
 |||  
 Db 35 GGGCCCAACCTGCTAGGATTTT 57

RESULT 11

ID AAH02411 standard; DNA; 100 BP.

XX AAH02411;

DT 12-JUN-2001 (first entry)

DE Human Factor XIII coding sequence fragment SEQ ID NO: 108.

KM Database; polymorphism; SNP; human; genetic marker; disease; infection;

XX drug response; ds.

OS Homo sapiens.

PN WO200127857-A2.

PD 19-APR-2001.

PF 13-OCT-2000; 2000WO-US028413.

PR 13-OCT-1999; 99US-0159176P.

PR 10-JUL-2000; 2000US-0217251P.

PR 10-JUL-2000; 2000US-0217658P.

PR 19-SEP-2000; 2000US-00663968.

PA (SEQU-) SEQUENOM INC.

PI Braun A, Koester H, Van Den Boom D, Ping Y, Rodi C, He L,

PI Chiu N, Jurinke C;

DR WPI; 2001-273865/28.

XX Producing a database for identifying polymorphic genetic markers,

PT comprises obtaining data relating to members of a healthy population and

PT entering the information into a database.

PS Example 9; Page 303; 304pp; English.

XX The present invention provides a database of human samples obtained from

CC healthy individuals which can be used to identify polymorphic genetic

CC markers. Data obtained for the database can be used to sort the samples

CC by parameters such as age, sex and ethnicity. This is useful in linking

CC markers with diseases, susceptibility to infection and drug responses.

CC The present sequence was used in an assay to demonstrate the uses of the

CC database of the invention

XX Sequence 100 BP; 23 A; 31 C; 28 G; 18 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 64.8%; Score 16.2; DB 4; Length 100;

XX Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGCGCAACCTGCTAGGAT 22

DB 64 GGGCGCAACCTGCAAGTAT 84

RESULT 12

AAH02412

AAH02412 standard; DNA; 100 BP.

AAH02412;

12-JUN-2001 (first entry)

Human Factor XIII coding sequence fragment SEQ ID NO: 109.

Database; polymorphism; SNP; human; genetic marker; disease; infection;

XX drug response; ds.

XX Homo sapiens.

XX WO200127857-A2.

XX 19-APR-2001.

XX 13-OCT-2000; 2000WO-US028413.

PR 13-OCT-1999; 99US-0159176P.

PR 10-JUL-2000; 2000US-0217251P.

PR 10-JUL-2000; 2000US-0217658P.

PR 19-SEP-2000; 2000US-00663968.

PA (SEQU-) SEQUENOM INC.

PI Braun A, Koester H, Van Den Boom D, Ping Y, Rodi C, He L,

PI Chiu N, Jurinke C;

DR WPI; 2001-273865/28.

XX Producing a database for identifying polymorphic genetic markers,

PT comprises obtaining data relating to members of a healthy population and

PT entering the information into a database.

PS Example 9; Page 303; 304pp; English.

XX The present invention provides a database of human samples obtained from

CC healthy individuals which can be used to identify polymorphic genetic

CC markers. Data obtained for the database can be used to sort the samples

CC by parameters such as age, sex and ethnicity. This is useful in linking

CC markers with diseases, susceptibility to infection and drug responses.

CC The present sequence was used in an assay to demonstrate the uses of the

CC database of the invention

XX Sequence 100 BP; 23 A; 31 C; 27 G; 19 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 64.8%; Score 16.2; DB 4; Length 100;

XX Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGCGCAACCTGCTAGGAT 22

DB 64 GGGCGCAACCTGCAAGTAT 84

RESULT 13

ACC00078/c

ACC00078 standard; DNA; 33 BP.

ACC00078;

26-JUN-2003 (first entry)

Primer #4 related to human retinoblastoma binding protein.

Human; retinoblastoma binding protein 34.54; tumour; ss; primer.

XX Homo sapiens.

XX CN1380303-A.

XX 20-NOV-2002.

XX 11-APR-2001; 2000CN-00125808.

XX 11-APR-2001; 2000CN-00125808.

XX 11-APR-2001; 2000CN-00125808.

XX (SHAN-) SHANGHAI BOWINDOW GENE DEV INC.

XX Mao Y, Xie Y,

XX WPI; 2003-222536/22.

XX A novel polypeptide-human retinoblastoma binding protein 34.54.

XX Example 4; Page 21; 35pp; Chinese.

XX The present invention relates to human retinoblastoma binding protein

CC 34.54, used to treat various tumours. The present sequence represents a

CC primer related to human retinoblastoma binding protein encoding sequence



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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 01:14:18 / Search time 1266.56 Seconds  
(without alignments)

589.436 Million cell updates/sec

Title: US-10-001-407-10

Perfect score: 25

Sequence: 1 cggcgccacacgcctcagggatttc 25

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 569238

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*  
1: em\_estbda:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estm:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_estc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_est6:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.6	62.4	62	14	CF885516 trico82xk
2	15.4	61.6	100	9	AA470378 nei10c02.s
3	14.4	57.6	82	9	A1256079 u194g12.x
4	14.4	57.6	92	14	CB165114 44 A1falf

Result No.	Score	Query Match	Length	ID	Description
5	14.2	56.8	62	9	A1669171
6	14.2	56.8	72	12	B057939
7	14.2	56.0	41	12	B1907426
8	14.2	56.0	96	6	AA065383
9	14.2	56.0	97	28	A2600786
10	13.8	55.2	64	29	CG399846
11	13.8	55.2	64	29	CL002253
12	13.8	55.2	73	14	U44135
13	13.8	55.2	75	14	F33772
14	13.8	55.2	84	12	BM126072
15	13.8	55.2	94	28	A2921627
16	13.6	54.4	45	14	CB209994
17	13.6	54.4	45	14	CB211074
18	13.6	54.4	45	14	CB213865
19	13.6	54.4	61	28	BH913033
20	13.6	54.4	76	9	AA566995
21	13.6	54.4	78	29	CG712371
22	13.6	54.4	81	28	B2380126
23	13.6	54.4	91	14	R82154
24	13.6	54.4	91	29	D86884
25	13.6	54.4	91	29	DME547093
26	13.6	54.4	92	29	HSNC24E11
27	13.6	54.4	100	28	B2595658
28	13.6	54.4	100	29	CG781268
29	13.4	53.6	49	9	AA513131
30	13.4	53.6	50	9	AU106807
31	13.4	53.6	57	29	CG717331
32	13.4	53.6	63	29	CG554070
33	13.4	53.6	66	29	CG712601
34	13.4	53.6	68	29	CG519780
35	13.4	53.6	79	9	AA778587
36	13.4	53.6	79	29	CG487857
37	13.4	53.6	80	29	AG217446
38	13.4	53.6	82	12	B1908831
39	13.4	53.6	82	29	AG219169
40	13.4	53.6	85	9	A1014256
41	13.4	53.6	96	13	B0816046
42	13.4	53.6	98	28	B2763567
43	13.2	52.8	77	9	AT006310
44	13.2	52.8	77	9	AA491818
45	13.2	52.8	91	14	CK108605

## ALIGNMENTS

RESULT 1  
CF885516 62 bp mRNA linear EST 31-OCT-2003  
LOCUS trico82xk23.b11 T.reesei mycelial culture, Version 6 October 2003  
DEFINITION Hypocrea jecorina CDNA clone trico82xk23, mRNA sequence.  
ACCESSION CF885516  
VERSION CF885516.1 GI:38140198  
KEYWORDS EST.  
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)  
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreales; Hypocrea.

REFERENCE  
1 (bases 1 to 62)  
Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D., Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and Dean, R.A.  
Analysis of the protein processing and secretion pathways in a Trichoderma reesei EST dataset  
Unpublished (2003)  
Contact: Ralph A. Dean  
Fungal Genomics Laboratory  
North Carolina State University  
Campus Box 7251, Raleigh, NC 27695, USA  
Tel: 919-513-0020  
Fax: 919-513-0024  
Email: ralph.dean@ncsu.edu  
Seq primer: UT-F1 primer.

# FEATURES

## source

Location/Qualifiers  
1..62  
/organism="Hypocrea jecorina"  
/mol\_type="mRNA"  
/strain="QM6a"  
/db\_xref="taxon:51453"  
/clone="tric082xk23"  
/dev\_stage="mycelia"  
/clone\_lib="T.reesei mycelial culture, Version 6 October 2003"  
/note="Vector: PREP3Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

# ORIGIN

Query Match 62.4%; Score 15.6; DB 14; Length 62;  
Best Local Similarity 81.8%; Pred. No. 1.1e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GCGCCAACTGCTGAGGATTTT 25  
40 GGACACCTGCTGAGGATTTT 61

RESULT 2 100 bp mRNA linear EST 13-NOV-1998  
AA470378  
LOCUS AA470378  
DEFINITION mRNA sequence.  
ACCESSION AA470378  
VERSION AA470378.1 GI:2197687  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Stransberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at: www-bio.illn.gov/bdrip/image/image.html  
Insert Length: 527 Std Error: 0.00  
Seq primer: -41ml3 fwd. RT from Amersham

High quality sequence stop: 86.  
Location/Qualifiers

# FEATURES

## source

1..100  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:880802"  
/sex="pooled"  
/tissue\_type="colon"  
/lab\_host="DH10B"  
/clone\_lib="NCI-CGAP\_C03"  
/note="Vector: PRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization."

# ORIGIN

Query Match 61.6%; Score 15.4; DB 9; Length 100;  
Best Local Similarity 76.0%; Pred. No. 1.6e+04;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGGCGCCAACTGCTGAGGATTTT 25  
71 CTGCGCCAACTGCTGAGGATTTT 47

RESULT 3 82 bp mRNA linear EST 12-NOV-1998  
A1256079  
LOCUS A1256079  
DEFINITION u194g12.x1 Sugano mouse liver m1a Mus musculus cDNA clone IMAGE:1890118.3 similar to SW:COX3\_RAT P05505 CYTOCHROME C OXIDASE POLYPEPTIDE III ; mRNA sequence.  
ACCESSION A1256079  
VERSION A1256079.1 GI:3863604  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 82)  
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Scheinberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelning, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
TITLE The WashU-HMI Mouse EST Project  
JOURNAL Unpublished (1996)  
COMMENT Contact: Maria W/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through ILNI; contact the IMAGE Consortium (info@image.lln.gov) for further information.  
MGI:974442  
Trace considered overall poor quality  
Possible reversed clone; similarity on wrong strand  
Seq primer: custom primer used  
High quality sequence stop: 1.  
Location/Qualifiers

# FEATURES

## source

1..82  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1890118"  
/sex="female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="Sugano mouse liver m1a"  
/note="Organ: liver; Vector: pMT185-FLJ; Site 1: DraIII (CACTGCTG); Site 2: DraIII (CACCAGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCTTACTGCG] and cloned into distinct DraIII sites of the pMT185-FLJ vector (5' site CACTGCTG, 3' site CACCAGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGCTCTTAAGCTGG and 3' end primer CGACCTGCACTGAGCACA."

# ORIGIN

Query Match 57.6%; Score 14.4; DB 9; Length 82;  
Best Local Similarity 75.0%; Pred. No. 4.2e+04;



Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGGGCCCACTGCTAGGATTTT 25

Db 4 GGGCTCCAAACCCCAAGGATGTT 27

# RESULT 4

CB165114/c

LOCUS 92 bp mRNA linear EST 30-JAN-2003

DEFINITION 44 Alfalfa developing flower bud library Medicago sativa cDNA, mRNA

ACCESSION

CB165114

VERSION

CB165114.1

KEYWORDS

EST

SOURCE

ORGANISM

Medicago sativa

Medicago sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosids; euroside I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;

Medicago.

1 (bases 1 to 92)

Barone, P., Rosellini, D. and Veronesi, P.

Isolation of expressed sequence tags from developing flowers of

female sterile and female fertile alfalfa plants

unpublished (2002)

CONTACT: Rosellini, D.

Dipartimento di Biologia Vegetale e Biotecnologie Agroambientali

University of Perugia

Borgo XX giugno 74, 06121, Perugia, Italy

Tel: +390755856211

Fax: +390755856224

Email: rosellini@unipg.it

POLYA=No.

Location/Qualifiers

1..92

/organism="Medicago sativa"

/mol\_type="mRNA"

/cultivar="B17 x P13 P1 population"

/db\_xref="taxon:3879"

/sex="hermaphrodite"

/dev\_stage="From ovule primordia to anthesis"

/lab\_host="B.colli"

/clone\_lib="Alfalfa developing flower bud library"

/note="Organ: Developing flower buds; Vector: Invitrogen

PCR4 TOPO Vector; This EST was obtained with the cDNA-AFLP

method (Bachem et al. Plant Journal 9:745-753, 1996). Total

RNA was extracted from three female fertile and three

female sterile alfalfa plants from an P1 population

obtained by crossing the plants B17 and P13 (Rosellini et

al. Theoretical and Applied Genetics, 97:1 289-1295,

1998). Equal amounts of RNA from each fertile or sterile

plant were b ulked and used for the cDNA-AFLP protocol.

The restriction endonucleases EcoRI and MseI were used.

Bands that were polymorphic between the female sterile and

female fertile bulks were isolated from the polyacrilamide

gel, cloned in a plasmid vector (Invitrogen PCR4 TOPO) and

sequenced using the M13F primer. The published sequence

begins and ends with the EcoRI (GAATTC) and MseI (TTAA)

recognition sequences, respectively. The technical help of

Francesco Panara is gratefully acknowledged."

## ORIGIN

Query Match 57.6%; Score 14.4; DB 14; Length 92;

Best Local Similarity 75.0%; Pred. No. 4.4e+04;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGGGCCCACTGCTAGGATTTT 25

Db 48 GGTAGTCAACTCTCTATAGATTTT 25

RESULT 5

AI669171/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 62)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapsb@nci.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbr/image/image.html

Seq primer: -40UP from Gibco.

Location/Qualifiers

1..62

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2312082"

/sex="male"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Pr28"

/note="Organ: prostate; Vector: pTZ19-Pac (Pharmacia)

with a modified polylinker; Plasmid DNA from the

normalized library NCI CGAP\_Pr22 was prepared, and 86

circles were made in vitro. Following HAP purification,

this DNA was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from a pool

of 5,000 clones made from the same library (cloneds

985608-986759, 110192-110195, and 121928-1220615).

Subtraction by Bento Soares and M. Fatima Bonaldo.

"

ORIGIN

Query Match 56.8%; Score 14.2; DB 9; Length 62;

Best Local Similarity 84.2%; Pred. No. 4.8e+04;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GCCAACCTGCTAGGATTTT 24

Db 56 GCCAACCTGCTAGGATTTT 38

## RESULT 6

BU057939

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Xenopus laevis

Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 72)

Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-I, T. and

Kohara, Y.

TITLE  
JOURNAL  
COMMENT

Expressed genes in X. laevis embryo  
Unpublished (2001)  
Contact: Tadashi Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshin@genes.nig.ac.jp  
The information of this clone is available through the following  
URL:  
http://xenopus.nibb.ac.jp.

FEATURES  
source

Location/Qualifiers  
1..72  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="X103003"  
/issue\_type="whole embryo"  
/dev\_stage="stage 25"  
/clone\_lib="NIBB Mochii normalized Xenopus tailbud  
library"

ORIGIN

Query Match 56.8%; Score 14.2; DB 12; Length 72;  
Best Local Similarity 72.7%; Pred. No. 5e+04;  
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GCGCCAACTGCTAGGATTTT 25  
17 GCGCCAACTTNTGGGATTTT 38

Db

RESULT 7  
BI907426 41 bp mRNA linear EST 16-OCT-2001  
LOCUS  
DEFINITION  
603063502F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5212728 5',  
mRNA sequence.

ACCESSION  
BI907426

VERSION  
BI907426.1 GI:16170258

KEYWORDS  
EST.

SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens

REFERENCE  
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS  
NIH-MGC http://mgc.ncl.nih.gov/.

TITLE  
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
Unpublished (1999)

COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cga@db-rcmail.nih.gov

FEATURES  
source

Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA sequencing by: Incyte Genomics, Inc.  
Cloned distribution: MGC clone distribution information can be  
http://image.llnl.gov  
Plate: LHM1534 row: C column: 01  
High quality sequence stop: 41.  
Location/Qualifiers

1..41

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5212728"

/issue\_type="leukocyte"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_118"

/note="Vector: pCMV-SPORT6, Site 1: NotI; Site 2: EcoRV  
(destroyed); RNA source leukocyte from anonymous pool of  
non-activated adult donors. Library is oligo-dT primed  
and directionally cloned (EcoRV site is destroyed upon

ORIGIN

Query Match 56.0%; Score 14; DB 12; Length 41;  
Best Local Similarity 77.3%; Pred. No. 5.2e+04;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GCGCCAACTGCTAGGATTT 24  
9 GCGCCAACTTCTCGGATCT 30

Db

RESULT 8  
AA065383/c 96 bp mRNA linear EST 03-FEB-1997  
LOCUS  
DEFINITION  
m51e06.r1 Stragene mouse testis (#37308) Mus musculus cDNA  
clone IMAGE:515554 5', mRNA sequence.

ACCESSION  
AA065383

VERSION  
AA065383.1 GI:1562664

KEYWORDS  
EST.

SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 96)  
Marrs M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,  
Geisler S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,  
Schellenberg R., Steptoe M., Tan F., Underwood K., Moore B.,  
Theisinger B., Wylie T., Lennon G., Soares B., Wilson R. and  
Waterston R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marrs M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -26ml3 rev1 ET from Amersham

High quality sequence stop: 90.

Location/Qualifiers

1..96

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="CD-1"

/db\_xref="taxon:10090"

/clone="IMAGE:515554"

/sex="males"

/issue\_type="testis"

/dev\_stage="10-12 week old"

/lab\_host="SOLR (kanamycin resistant)"

/clone\_lib="Stratagene mouse testis (#37308)"

/note="Organ: testis; Vector: pBluescript SK-; Site 1:  
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:  
-5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor  
sequence: 5' CTCGAGTCTTTTCTTTT 3' "

ORIGIN

Query Match 56.0%; Score 14; DB 9; Length 96;  
Best Local Similarity 77.3%; Pred. No. 6.7e+04;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GCGCCAACTGCTAGGATTT 24  
||||| ||| |||



JOURNAL  
COMMENT

population  
Unpublished (2003)  
Contact: Donald R. McCarty  
Plant Molecular and Cellular Biology Program  
University of Florida  
PO 110690 Gainesville, FL 32611-0690, USA  
Tel: 352-392-1928 x322  
Email: drmc@ufl.edu  
Sequence flanking probable Mu insertion site in UniformMu line:  
0280069-08, primer set: C  
Classes: transposon insertion site.  
Location/Qualifiers  
1. .64  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="W22 (ACR, bz1-m3)"  
/db\_xref="taxon:4577"  
/clone="0280069-08C1-G08"  
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon  
insertions in Mu inactive lines were extracted from the  
UniformMu maize population by the thermo asymmetric  
interlaced PCR (TAIL) protocol using primers specific for  
the Mu terminal inverted repeat and a set of 16 arbitrary  
primers. Amplicons were size enriched using Sepharose 400  
spin columns and cloned into the TOPO PCR4 vector."

FEATURES  
source

## ORIGIN

## Query Match

Best Local Similarity 55.2%; Score 13.8; DB 29; Length 64;  
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CGGCGCCCAACCTGCTAGGATTT 25  
Db 63 CGGTGTCCACTCCTAGGATTT 39

## RESULT 12

## LOCUS

## U44135

## DEFINITION

ENU44135 *Aspergillus nidulans* cleistothecium linear EST 03-Apr-1996

## ACCESSION

## U44135

## VERSION

## U44135.1

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

Contact: Keon-Sang Chae  
Chonbuk National University  
Chonju, 561-756, S. Korea  
Tel: +82-652-70-3340  
Fax: +82-652-70-3345  
Email: chae@chonbuknms.chonbuk.ac.kr.  
Location/Qualifiers  
1. .73  
/organism="Emmericella nidulans"  
/mol\_type="mRNA"  
/strain="FGSC4"  
/db\_xref="taxon:162425"  
/clone="SR0101"  
/issue\_type="cleistothecium"  
/cell\_type="hull cell"  
/dev\_stage="sexual"

## ORIGIN

/clone\_1lb="Aspergillus nidulans cleistothecium"  
/note="3'-directed cDNA clones; single-pass sequencing"

## Query Match

Best Local Similarity 55.2%; Score 13.8; DB 14; Length 73;  
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CGGCGCCCAACCTGCTAGGATTT 25  
Db 15 CGGTGTCCACTCCTAGGATTT 39

## RESULT 13

## LOCUS

## F33772

## DEFINITION

HSP27429 HM3 Homo sapiens cDNA clone s300010H07, mRNA sequence.

## ACCESSION

## F33772

## VERSION

## F33772.1

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

## source

Contact: Valle G.  
CIRI Biotechnology Centre  
University of Padua  
Via Trieste 75, 35121 Padua, Italy  
ABI Chromatograms and other information are available on WWW at  
http://gryp.bio.unipd.it.  
Location/Qualifiers  
1. .75  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="s300010H07"  
/sex="female"  
/issue\_type="pectoral muscle (after mastectomy)"  
/note="Vector: pCDNAII (Invitrogen); Site 1: BstXI;  
Site 2: NotI. The library was constructed by G. Valle.  
The first strand cDNA was primed with a biotinylated  
oligo-dT-NotI primer  
(5'-biotin-AACCTGGCTGAGCGCGCTTTTCTTTTCTTTT-3'). The  
350-550 bp. The 3' specific fragments were selected by  
streptavidin coated magnetic beads, ligated to  
non-palindromic BstXI adapters, NotI digested and  
directionally cloned into BstXI-NotI cut pCDNAII vector."

## ORIGIN

## Query Match

Best Local Similarity 55.2%; Score 13.8; DB 14; Length 75;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCGCGCAACCTGCTAGG 19  
Db 5 GCGCGCAACCTGCTAGG 21

## RESULT 14

## LOCUS

## BM126072

## 84 bp

## mRNA

## linear

## EST 12-MAR-2002



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GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 01:28:53 ; Search time 39.2857 Seconds

(without alignments)  
353.151 Million cell updates/sec

Title: US-10-001-407-10

Perfect score: 25

Sequence: 1 CGGGCGCAACCTGCTGCTT 25

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 939230

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

1: /cgn2\_6/prodata/2/ina/5A.COMB.seq.\*  
2: /cgn2\_6/prodata/2/ina/5B.COMB.seq.\*  
3: /cgn2\_6/prodata/2/ina/6A.COMB.seq.\*  
4: /cgn2\_6/prodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/prodata/2/ina/PCUTS.COMB.seq.\*  
6: /cgn2\_6/prodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	68.0	22	3	US-09-102-830-31 Sequence 31, Appl
2	16.6	66.4	42	1	US-08-105-483-160 Sequence 160, App
3	16.6	66.4	42	1	US-08-709-209-160 Sequence 160, App
4	16.6	66.4	42	1	US-08-303-275-48 Sequence 48, Appl
5	16.6	66.4	42	1	US-08-458-101-160 Sequence 160, Appl
6	15.4	61.6	33	2	US-08-455-968E-62 Sequence 62, Appl
7	15.4	61.6	33	4	US-09-758-282B-151 Sequence 151, App
8	15.4	61.6	37	4	US-09-552-950-22 Sequence 22, Appl
9	14.4	57.6	70	4	US-09-393-171-22 Sequence 22, Appl
10	14.2	56.8	24	1	US-08-068-945A-13 Sequence 13, Appl
11	14.2	56.8	24	1	US-08-442-806-13 Sequence 13, Appl
12	14.2	56.8	35	1	US-08-748-068-14 Sequence 14, Appl
13	14	56.0	65	4	US-09-625-188-27 Sequence 27, Appl
14	13.8	55.2	38	1	US-08-137-175A-18 Sequence 18, Appl
15	13.8	55.2	38	3	US-08-479-017-18 Sequence 18, Appl
16	13.8	55.2	60	1	US-08-441-430-12 Sequence 12, Appl
17	13.8	55.2	70	3	US-09-306-405-20 Sequence 20, Appl
18	13.6	54.4	61	3	US-08-463-682-22 Sequence 22, Appl
19	13.4	53.6	26	4	US-09-495-066-10 Sequence 10, Appl
20	13.4	53.6	48	2	US-08-418-848A-23 Sequence 23, Appl
21	13.4	53.6	49	1	US-08-706-135-3 Sequence 3, Appl
22	13.4	53.6	49	5	PCT-US95-16804-3 Sequence 3, Appl
23	13.2	52.8	62	3	US-08-443-950-1 Sequence 1, Appl
24	13.2	52.8	67	4	US-09-650-324A-64 Sequence 64, Appl
25	13	52.0	27	4	US-09-234-827B-10 Sequence 10, Appl
26	13	52.0	31	1	US-08-019-870-33 Sequence 33, Appl
27	13	52.0	50	4	US-09-475-947A-186 Sequence 186, App

28	13	52.0	96	3	US-08-484-322-31 Sequence 31, Appl
29	12.8	51.2	27	4	US-09-439-616-8 Sequence 8, Appl
30	12.8	51.2	38	4	US-09-233-086-12 Sequence 12, Appl
31	12.8	51.2	47	4	US-09-422-978-739 Sequence 739, Appl
32	12.8	51.2	78	1	US-08-639-763-14 Sequence 14, Appl
33	12.8	51.2	78	4	US-09-171-755B-14 Sequence 14, Appl
34	12.8	51.2	84	2	US-08-476-176B-23 Sequence 23, Appl
35	12.8	51.2	84	3	US-08-127-721A-23 Sequence 23, Appl
36	12.8	51.2	84	3	US-08-485-246A-23 Sequence 23, Appl
37	12.8	51.2	97	3	US-08-836-561-56 Sequence 56, Appl
38	12.8	51.2	97	4	US-09-434-122-56 Sequence 56, Appl
39	12.6	50.4	20	3	US-08-866-340-49 Sequence 49, Appl
40	12.6	50.4	20	3	US-09-103-875-55 Sequence 55, Appl
41	12.6	50.4	33	4	US-09-336-845B-64 Sequence 64, Appl
42	12.6	50.4	34	4	US-08-387-805-14 Sequence 14, Appl
43	12.6	50.4	36	3	US-09-113-750A-48 Sequence 48, Appl
44	12.6	50.4	78	2	US-08-829-876-22 Sequence 22, Appl
45	12.6	50.4	78	4	US-09-234-874A-22 Sequence 22, Appl

## ALIGNMENTS

RESULT 1  
US-09-102-830-31  
Sequence 31, Application US/09102830  
Patent No. 6001558  
GENERAL INFORMATION:  
APPLICANT: BACKUS, JOHN W  
APPLICANT: ATWOOD, SUSAN M  
APPLICANT: CASEY, ANN E  
APPLICANT: RASMUSSEN, ERIC B  
APPLICANT: CUMMINS, THOMAS J  
TITLE OF INVENTION: AMPLIFICATION AND DETECTION OF HIV-1  
TITLE OF INVENTION: AND/OR HIV-2  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JOHNSON & JOHNSON  
STREET: ONE JOHNSON & JOHNSON PLAZA  
CITY: NEW BRUNSWICK  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 08933  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09102,830  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: OGDEN, STASIA L  
REGISTRATION NUMBER: 36,228  
REFERENCE/DOCKET NUMBER: CDS-137/SLO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-524-2819  
TELEFAX: 908-524-2808  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-102-830-31  
Query Match 68.0%; Score 17; DB 3; Length 22;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0;  
Indels 0; Gaps 0;  
1 CGGGCGCAACCTGCTGCTT 17

Db 6 CGGCGCCACCTGCTA 22

RESULT 2  
US-08-105-483-160

Sequence 160, Application US/08105483  
Patent No. 5494807

GENERAL INFORMATION:

APPLICANT: Paolletti, Enzo

TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE

NUMBER OF SEQUENCES: 462

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford

STREET: 530 Fifth Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/105,483

FILING DATE: 12-AUG-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/847,951

FILING DATE: 06-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454310-2400

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333

TELEFAX: (212) 840-0712

INFORMATION FOR SEQ ID NO: 160:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-105-483-160

Query Match

Best Local Similarity 66.4%; Score 16.6; DB 1; Length 42;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGCGCCACCTGCTAGGATTT 24

Db 9 GGGCATCAGCAGCTAGGATTT 31

US-08-709-209-160

Sequence 160, Application US/08709209

Patent No. 5762938

GENERAL INFORMATION:

APPLICANT: Paolletti, Enzo

TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE

NUMBER OF SEQUENCES: 462

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford

STREET: 530 Fifth Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/709,209

FILING DATE: 21-AUG-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/105,483

FILING DATE: 12-AUG-1993

APPLICATION NUMBER: US 07/847,951

FILING DATE: 06-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454310-2400

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333

TELEFAX: (212) 840-0712

INFORMATION FOR SEQ ID NO: 160:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-709-209-160

Query Match

Best Local Similarity 66.4%; Score 16.6; DB 1; Length 42;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGCGCCACCTGCTAGGATTT 24

Db 9 GGGCATCAGCAGCTAGGATTT 31

US-08-303-275-48

Sequence 48, Application US/08303275

Patent No. 576598

GENERAL INFORMATION:

APPLICANT: Paolletti, Enzo

APPLICANT: Taregilla, James

TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS RECOMBINANT

NUMBER OF SEQUENCES: 205

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford

STREET: 530 Fifth Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/303,275

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/897,382

FILING DATE: 11-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506



REFERENCE/DOCKET NUMBER: 454310-2420  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-303-275-48

Query Match 66.4%; Score 16.6; DB 1; Length 42;  
Best Local Similarity 82.6%; Pred. No. 22;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGGCCCACTGCTAGGATTT 24  
Db 9 GGGCATCAGCAGCTAGGATTT 31

RESULT 5  
US-08-458-101-160  
Sequence 160, Application US/08458101  
Patent No. 5766599  
GENERAL INFORMATION:  
APPLICANT: Paolucci, Enzo  
APPLICANT: Perkins, Marion E.  
APPLICANT: Taylor, Jill  
APPLICANT: Tartaglia, James  
APPLICANT: No. 5766599ton, Elizabeth K.  
APPLICANT: de Taisne, Charles  
APPLICANT: Limbach, Keith J.  
APPLICANT: Johnson, Gerard P.  
APPLICANT: Pincus, Steven E.  
APPLICANT: Cox, William I.  
APPLICANT: Audonnet, Jean-Christophe Francis  
APPLICANT: Gettig, Russell Robert  
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE  
TITLE OF INVENTION: STRAIN  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o William S. Frommer  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458.101  
FILING DATE: 01-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2740  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 160:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-458-101-160

Query Match 66.4%; Score 16.6; DB 1; Length 42;  
Best Local Similarity 82.6%; Pred. No. 22;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 GGGGCCCACTGCTAGGATTT 24  
Db 9 GGGCATCAGCAGCTAGGATTT 31

RESULT 6  
US-08-455-968B-62/c  
Sequence 62, Application US/08455968B  
Patent No. 5874283  
GENERAL INFORMATION:  
APPLICANT: Harrington, John L.  
APPLICANT: Hsieh, Chih-Lin  
APPLICANT: Lieber, Michael  
TITLE OF INVENTION: Mammalian Flap-Specific Endonuclease  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455.968B  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 18985-000100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (oligonucleotide)  
US-08-455-968B-62  
Query Match 61.6%; Score 15.4; DB 2; Length 33;  
Best Local Similarity 76.0%; Pred. No. 86;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 GGGGCCCACTGCTAGGATTT 25  
Db 31 GCACCTGCACCTGCTAGGATTT 7  
RESULT 7  
US-09-758-282B-151  
Sequence 151, Application US/09758282B  
Patent No. 6635463  
GENERAL INFORMATION:  
APPLICANT: Ma, Wu-Po  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Kaiser, Michael W.  
APPLICANT: Lyamicheva, Natalie E.  
APPLICANT: Allawi, Hatim T.  
APPLICANT: Schaefer, James J.  
APPLICANT: Neri, Bruce P.

```

/ TITLE OF INVENTION: Enzymes for the Detection of Nucleic Acid Sequences
/ FILE REFERENCE: FORS 04931
/ CURRENT APPLICATION NUMBER: US/09/758,282B
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 09/577,304
/ PRIOR FILING DATE: 2000-05-24
/ NUMBER OF SEQ ID NOS: 280
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 151
/ LENGTH: 33
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-758-282B-151

Query Match      61.6% Score 15.4; DB 4; Length 33;
Best Local Similarity 94.1%; Pred. No. 86;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 CGGCACTGCTAGGGA 21
Db      3 CGGCACTGCTAGGGA 19

RESULT 8
US-09-552-950-22
/ Sequence 22, Application US/09552950
/ Patent No. 6541248
/ GENERAL INFORMATION:
/ APPLICANT: Oxford Biomedica (UK) Limited
/ TITLE OF INVENTION: Anti-Viral Vectors
/ FILE REFERENCE: 674524-2004
/ CURRENT APPLICATION NUMBER: US/09/552,950
/ CURRENT FILING DATE: 2000-04-20
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 37
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:primer RIB3
US-09-552-950-22

Query Match      61.6% Score 15.4; DB 4; Length 37;
Best Local Similarity 76.0%; Pred. No. 88;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 CGGGCGCCACTGCTAGGATTTT 25
Db      12 CGGGCGCCACTGCTAGGATTTT 36

RESULT 9
US-09-393-171-22
/ Sequence 22, Application US/09393171
/ Patent No. 6673569
/ GENERAL INFORMATION:
/ APPLICANT: KUROKAWA, Yoichi
/ APPLICANT: YANAGI, Hideki
/ APPLICANT: YURA, Takashi
/ TITLE OF INVENTION: Dsba/Dsbb/Dsbc/Dsbd expression plasmid
/ FILE REFERENCE: 1422-391P
/ CURRENT APPLICATION NUMBER: US/09/393,171
/ CURRENT FILING DATE: 1999-09-09
/ EARLIER APPLICATION NUMBER: JP 10/255702
/ EARLIER FILING DATE: 1998-09-09
/ NUMBER OF SEQ ID NOS: 25
/ SEQ ID NO 22
/ LENGTH: 70
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
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US-09-393-171-22

Query Match      57.6% Score 14.4; DB 4; Length 70;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      2 GGGCGCACTGCTAGGATTTT 25
Db      3 GGGCGCACTGCTAGGATTTT 26

RESULT 10
US-08-068-945A-13/C
/ Sequence 13, Application US/08068945A
/ Patent No. 5616483
/ GENERAL INFORMATION:
/ APPLICANT: Bjursell, Gunnar
/ APPLICANT: Carlsson, Peter
/ APPLICANT: Enerback, Sven
/ APPLICANT: Hansson, Lennart
/ APPLICANT: Lidberg, Ulf
/ APPLICANT: Nilsson, Jeanette
/ APPLICANT: Tornell, Jan
/ TITLE OF INVENTION: New DNA Sequences
/ NUMBER OF SEQUENCES: 58
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: White & Case
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: United States
/ ZIP: 10036-2787
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/068,945A
/ FILING DATE: 27-MAY-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: SE 9201809-2
/ FILING DATE: 11-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: SE 9201826-6
/ FILING DATE: 12-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: SE 9202088-2
/ FILING DATE: 03-JUL-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: SE 9300902-5
/ FILING DATE: 19-MAR-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Steiner, Richard J.
/ REGISTRATION NUMBER: 35,372
/ REFERENCE/DOCKET NUMBER: 1103326-052
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)819-8783
/ TELEFAX: (212)354-8113
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 24 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-068-945A-13

Query Match      56.8% Score 14.2; DB 1; Length 24;
Best Local Similarity 84.2%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 3 GCGGCCCAACTGCTAGGGA 21  
|||||  
Db 24 GCGGCCCAACTGCTAGGGA 6

RESULT 11  
US-08-442-806-13/c  
; Sequence 13, Application US/08442806  
; Patent No. 5716817  
; GENERAL INFORMATION:  
; APPLICANT: Bjursell, Gunnar  
; APPLICANT: Carlsson, Peter  
; APPLICANT: Enerback, Sven  
; APPLICANT: Hansson, Lennart  
; APPLICANT: Lidberg, Ulf  
; APPLICANT: Nilsson, Jeanette  
; APPLICANT: Tornell, Jan  
; TITLE OF INVENTION: Genomic DNA Sequences  
; TITLE OF INVENTION: Encoding Human BSL/CEL  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: White & Case  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 10036-2787  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/442,806  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/068,945  
; FILING DATE: 27-MAY-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: SE 9201809-2  
; FILING DATE: 11-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: SE 9201826-6  
; FILING DATE: 12-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: SE 9202088-2  
; FILING DATE: 03-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: SE 9300902-5  
; FILING DATE: 19-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sterner, Richard J.  
; REGISTRATION NUMBER: 35,372  
; REFERENCE/DOCKET NUMBER: 1103326-052  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)819-8783  
; TELEFAX: (212)354-8113  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-442-806-13

Query Match 56.8%; Score 14.2; DB 1; Length 24;  
Best Local Similarity 84.2%; Pred. No. 3.3e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGGCCCAACTGCTAGGGA 21

Db 24 GCGGCCCAACTGCTAGGGA 6  
|||||

RESULT 12  
US-08-748-068-14  
; Sequence 14, Application US/08748068  
; Patent No. 5770410  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Chiral Synthesis  
; NUMBER OF SEQUENCES: 15  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/748,068  
; FILING DATE: 12-NOV-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256,959  
; FILING DATE: 05-OCT-1994  
; APPLICATION NUMBER: GB 92 02033.8  
; FILING DATE: 30-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 92 04702.6  
; FILING DATE: 04-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 93/00204  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 35 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-748-068-14

Query Match 56.8%; Score 14.2; DB 1; Length 35;  
Best Local Similarity 84.2%; Pred. No. 3.5e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGGCCCAACTGCTAGG 19  
|||||  
Db 6 GCGGCCCAACTGGAAG 24

RESULT 13  
US-09-625-188-27  
; Sequence 27, Application US/09625188  
; Patent No. 6307037  
; GENERAL INFORMATION:  
; APPLICANT: No. 6307037artis AG  
; TITLE OF INVENTION: Fungal Target Genes and Methods  
; FILE REFERENCE: PB/5-31285P1  
; CURRENT APPLICATION NUMBER: US/09/625,188  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 65  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: oligonucleotide  
; US-09-625-188-27

Query Match 56.0%; Score 14; DB 4; Length 65;  
Best Local Similarity 77.3%; Pred. No. 5e+02;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 CGGGGCCCACTGCTAGGAT 22  
Db 33 CGGTCTAGTCTCTCTAGGAT 54

## RESULT 14

US-08-137-175A-18/C  
; Sequence 18, Application US/08137175A  
; Patent No. 5777095  
; GENERAL INFORMATION:  
; APPLICANT: BARBOUR, Alan G.  
; APPLICANT: BERGSTROM, Sven  
; APPLICANT: HANSSON, Lennart  
; TITLE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDOFFERI AND  
; TITLE OF INVENTION: PROPHYLAXIS  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,175A  
; FILING DATE: 26-OCT-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/08972  
; FILING DATE: 22-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOPER, Iver P.  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/DOCKET NUMBER: BARBOUR=1B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 38 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-137-175A-18

Query Match 55.2%; Score 13.8; DB 1; Length 38;  
Best Local Similarity 88.2%; Pred. No. 5.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 8 CAACCTGCTAGGATTT 24  
Db 20 CAACCTGCTAGCGAATT 4

## RESULT 15

US-08-479-017-18/C  
; Sequence 18, Application US/08479017  
; Patent No. 6143872  
; GENERAL INFORMATION:  
; APPLICANT: BARBOUR, Alan G.  
; APPLICANT: BERGSTROM, Sven  
; APPLICANT: HANSSON, Lennart  
; TITLE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDOFFERI AND  
; TITLE OF INVENTION: PROPHYLAXIS  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/479,017  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,175  
; FILING DATE: 26-OCT-1993  
; APPLICATION NUMBER: PCT/US92/08972  
; FILING DATE: 22-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOPER, Iver P.  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/DOCKET NUMBER: BARBOUR=1B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 38 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-479-017-18

Query Match 55.2%; Score 13.8; DB 3; Length 38;  
Best Local Similarity 88.2%; Pred. No. 5.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 8 CAACCTGCTAGGATTT 24  
Db 20 CAACCTGCTAGCGAATT 4

Search completed: August 31, 2004, 04:43:17  
Job time : 40.2857 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 01:37:23 ; Search time 1822.08 Seconds  
(without alignments)  
67.525 Million cell updates/sec

Title: US-10-001-407-10

Perfect score: 25

Sequence: 1 CGGGCGCAACCTCTAGGATTTT 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3237270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 2018620

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
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8: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	25	100.0	25	14	US-10-001-407-10
2	25	100.0	34	14	US-10-001-407-8
3	25	100.0	34	14	US-10-001-407-9
4	25	100.0	52	14	US-10-001-407-15
5	18	72.0	25	14	US-10-001-407-14
6	18	72.0	58	14	US-10-001-407-19
7	16.6	66.4	24	14	US-10-001-407-13
8	16.6	66.4	57	14	US-10-001-407-18
9	16.2	64.8	100	15	US-10-272-665-108
10	16.2	64.8	100	15	US-10-272-665-109
11	16.2	64.8	100	15	US-10-273-321-108
12	16.2	64.8	100	15	US-10-273-321-109
13	16.2	64.8	100	15	US-10-272-756-108
14	16.2	64.8	100	15	US-10-272-756-109

15	16.2	64.8	100	16	US-10-273-228-108	Sequence 108, App
16	16.2	64.8	100	16	US-10-273-228-109	Sequence 109, App
17	15.4	61.6	33	10	US-09-864-636A-292	Sequence 292, App
18	15.4	61.6	33	10	US-09-758-282-151	Sequence 151, App
19	15.4	61.6	33	11	US-09-864-426A-292	Sequence 292, App
20	15.4	61.6	33	15	US-10-084-839-292	Sequence 292, App
21	15.4	61.6	37	9	US-09-999-183-21	Sequence 21, App
22	15.4	61.6	37	16	US-10-351-838-22	Sequence 22, App
23	15.2	60.8	95	15	US-10-126-474A-12	Sequence 12, App
24	14.8	59.2	20	15	US-10-126-474A-11	Sequence 11, App
25	14.4	57.6	65	15	US-10-251-364-23	Sequence 23, App
26	14.4	57.6	65	16	US-10-351-196-24	Sequence 24, App
27	14.4	57.6	65	16	US-10-463-980-26	Sequence 26, App
28	14.4	57.6	86	16	US-10-379-992A-10	Sequence 10, App
29	14.4	57.6	90	14	US-10-003-035-74	Sequence 74, App
30	14.4	57.6	90	15	US-10-286-332A-74	Sequence 74, App
31	14.4	57.6	90	16	US-10-280-915-74	Sequence 74, App
32	14.2	56.8	67	10	US-09-331-325A-99	Sequence 99, App
33	14.2	56.8	67	10	US-09-330-915A-140	Sequence 140, App
34	14.2	56.8	67	15	US-10-082-014-255	Sequence 255, App
35	14.2	56.8	67	15	US-10-372-076-285	Sequence 285, App
36	14.2	56.8	67	17	US-10-806-006-140	Sequence 140, App
37	14.2	56.8	67	17	US-10-677-074-285	Sequence 285, App
38	14.2	56.8	67	17	US-10-805-913-140	Sequence 140, App
39	14.2	56.8	75	10	US-09-331-325A-98	Sequence 98, App
40	14.2	56.8	75	15	US-10-082-014-254	Sequence 254, App
41	14.2	56.8	75	15	US-10-372-076-284	Sequence 284, App
42	14.2	56.8	75	17	US-10-806-006-139	Sequence 139, App
43	14.2	56.8	75	17	US-10-677-074-284	Sequence 284, App
44	14.2	56.8	75	17	US-10-805-913-139	Sequence 139, App
45	14.2	56.8	75	17	US-10-805-913-139	Sequence 139, App

#### ALIGNMENTS

RESULT 1  
US-10-001-407-10  
; Sequence 10, Application US/10001407  
; Publication No. US2002017127A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Yeasing  
; APPLICANT: Burrell, Terrie  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP117-03.UT  
; CURRENT APPLICATION NUMBER: US/10/001.407  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 60/242,620  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/280,058  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: HIV-2  
US-10-001-407-10

Query Match 100.0%; Score 25; DB 14; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.0091;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCGCAACCTCTAGGATTTT 25  
Db 1 CGGGCGCAACCTCTAGGATTTT 25

RESULT 2  
US-10-001-407-8/c  
; Sequence 8, Application US/10001407  
; Publication No. US2002017127A1

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/ GENERAL INFORMATION:
/ APPLICANT: Yang, Yeasing
/ APPLICANT: Burrell, Terrie
/ TITLE OF INVENTION: Compositions and Methods for Detecting
/ FILE REFERENCE: GP117-03.UT
/ CURRENT FILING DATE: 2001-10-22
/ PRIOR APPLICATION NUMBER: 60/242,620
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/280,058
/ PRIOR FILING DATE: 2001-03-30
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 8
/ LENGTH: 34
/ TYPE: DNA
/ ORGANISM: HIV-2
US-10-001-407-8
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Query Match          100.0%; Score 25; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CGGGCGCCAACTGCTAGGATTTT 25
DB 25 CGGGCGCCAACTGCTAGGATTTT 1
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RESULT 3
US-10-001-407-9
/ Sequence 9, Application US/10001407
/ Publication No. US20020177127A1
/ GENERAL INFORMATION:
/ APPLICANT: Yang, Yeasing
/ APPLICANT: Burrell, Terrie
/ TITLE OF INVENTION: Compositions and Methods for Detecting
/ FILE REFERENCE: GP117-03.UT
/ CURRENT FILING DATE: 2001-10-22
/ PRIOR APPLICATION NUMBER: 60/242,620
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/280,058
/ PRIOR FILING DATE: 2001-03-30
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 9
/ LENGTH: 34
/ TYPE: DNA
/ ORGANISM: HIV-2
US-10-001-407-9
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Query Match          100.0%; Score 25; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 CGGGCGCCAACTGCTAGGATTTT 25
DB 10 CGGGCGCCAACTGCTAGGATTTT 34
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RESULT 4
US-10-001-407-15
/ Sequence 15, Application US/10001407
/ Publication No. US20020177127A1
/ GENERAL INFORMATION:
/ APPLICANT: Yang, Yeasing
/ APPLICANT: Burrell, Terrie
/ TITLE OF INVENTION: Compositions and Methods for Detecting
/ FILE REFERENCE: GP117-03.UT
/ CURRENT FILING DATE: 2001-10-22
/ PRIOR APPLICATION NUMBER: 60/242,620
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/280,058
/ PRIOR FILING DATE: 2001-03-30
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 14
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: HIV-2
US-10-001-407-14
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/ CURRENT FILING DATE: 2001-10-22
/ PRIOR APPLICATION NUMBER: 60/242,620
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/280,058
/ PRIOR FILING DATE: 2001-03-30
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 15
/ LENGTH: 52
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: T7 promoter primer having a promoter sequence
/ OTHER INFORMATION: appended at the 5' end of an HIV-2 complementary
US-10-001-407-15
```

```
Query Match          100.0%; Score 25; DB 14; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CGGGCGCCAACTGCTAGGATTTT 25
DB 28 CGGGCGCCAACTGCTAGGATTTT 52
```

```
RESULT 5
US-10-001-407-14
/ Sequence 14, Application US/10001407
/ Publication No. US20020177127A1
/ GENERAL INFORMATION:
/ APPLICANT: Yang, Yeasing
/ APPLICANT: Burrell, Terrie
/ TITLE OF INVENTION: Compositions and Methods for Detecting
/ FILE REFERENCE: GP117-03.UT
/ CURRENT FILING DATE: 2001-10-22
/ PRIOR APPLICATION NUMBER: 60/242,620
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/280,058
/ PRIOR FILING DATE: 2001-03-30
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 14
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: HIV-2
US-10-001-407-14
```

```
Query Match          72.0%; Score 18; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CGGGCGCCAACTGCTAG 18
DB 8 CGGGCGCCAACTGCTAG 25
```

```
RESULT 6
US-10-001-407-19
/ Sequence 19, Application US/10001407
/ Publication No. US20020177127A1
/ GENERAL INFORMATION:
/ APPLICANT: Yang, Yeasing
/ APPLICANT: Burrell, Terrie
/ TITLE OF INVENTION: Compositions and Methods for Detecting
/ FILE REFERENCE: GP117-03.UT
/ CURRENT FILING DATE: 2001-10-22
/ PRIOR APPLICATION NUMBER: 60/242,620
/ PRIOR FILING DATE: 2000-10-23
```

PRIOR APPLICATION NUMBER: 60/280,058  
PRIOR FILING DATE: 2001-03-30  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 19  
LENGTH: 58  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: T7 promoter primer having a promoter sequence  
OTHER INFORMATION: appended at the 5' end of an HIV-2 complementary  
OTHER INFORMATION: primer sequence  
US-10-001-407-19

Query Match 72.0%; Score 18; DB 14; Length 58;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGGCGCCACCTGCTAG 18  
DB 41 CGGGCGCCACCTGCTAG 58

## RESULT 7

US-10-001-407-13  
Sequence 13, Application US/10001407  
Publication No. US20020177127A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Yeasing  
APPLICANT: Burrell, Terrie  
TITLE OF INVENTION: Compositions and Methods for Detecting  
TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)  
FILE REFERENCE: GP117-03-UT  
CURRENT APPLICATION NUMBER: US/10/001,407  
CURRENT FILING DATE: 2001-10-22  
PRIOR APPLICATION NUMBER: 60/242,620  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/280,058  
PRIOR FILING DATE: 2001-03-30  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 13  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer mismatches HIV-2 sequence by deletion of  
OTHER INFORMATION: one nucleotide  
US-10-001-407-13

Query Match 66.4%; Score 16.6; DB 14; Length 24;  
Best Local Similarity 82.6%; Pred. No. 1.8e+02;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 GGGCGCCACCTGCTAGGATTT 25  
DB 2 GGGCGCCACCTGCTAGGATTT 24

## RESULT 8

US-10-001-407-18  
Sequence 18, Application US/10001407  
Publication No. US20020177127A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Yeasing  
APPLICANT: Burrell, Terrie  
TITLE OF INVENTION: Compositions and Methods for Detecting  
TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)  
FILE REFERENCE: GP117-03-UT  
CURRENT APPLICATION NUMBER: US/10/001,407  
CURRENT FILING DATE: 2001-10-22  
PRIOR APPLICATION NUMBER: 60/242,620  
PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/280,058  
PRIOR FILING DATE: 2001-03-30  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 18  
LENGTH: 57  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: T7 promoter primer having a promoter sequence  
OTHER INFORMATION: appended at the 5' end of the sequence given as  
OTHER INFORMATION: SEQ ID NO:13  
US-10-001-407-18

Query Match 66.4%; Score 16.6; DB 14; Length 57;  
Best Local Similarity 82.6%; Pred. No. 1.9e+02;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 GGGCGCCACCTGCTAGGATTT 25  
DB 35 GGGCGCCACCTGCTAGGATTT 57

## RESULT 9

US-10-272-665-108  
Sequence 108, Application US/10272665  
Publication No. US20030180748A1  
GENERAL INFORMATION:  
APPLICANT: Braun et al.  
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POI  
TITLE OF INVENTION: GENETIC MARKERS  
FILE REFERENCE: 24736-2033E  
CURRENT APPLICATION NUMBER: US/10/272,665  
CURRENT FILING DATE: 2002-10-15  
PRIOR APPLICATION NUMBER: 09/687,483  
PRIOR FILING DATE: 2000-07-10  
PRIOR APPLICATION NUMBER: 60/217,658  
PRIOR FILING DATE: 2000-07-10  
PRIOR APPLICATION NUMBER: 60/159,176  
PRIOR FILING DATE: 1999-10-13  
PRIOR APPLICATION NUMBER: 60/217,251  
PRIOR FILING DATE: 2000-07-10  
PRIOR APPLICATION NUMBER: 09/663,968  
PRIOR FILING DATE: 2000-09-19  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 108  
LENGTH: 100  
TYPE: DNA  
ORGANISM: Hom sapien  
US-10-272-665-108

Query Match 64.8%; Score 16.2; DB 15; Length 100;  
Best Local Similarity 85.7%; Pred. No. 3.1e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GGGCGCCACCTGCTAGGAT 22  
DB 64 GGGCGTCACCTGCAAGGAT 84

## RESULT 10

US-10-272-665-109  
Sequence 109, Application US/10272665  
Publication No. US20030180748A1  
GENERAL INFORMATION:  
APPLICANT: Braun et al.  
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POI  
TITLE OF INVENTION: GENETIC MARKERS  
FILE REFERENCE: 24736-2033E  
CURRENT APPLICATION NUMBER: US/10/272,665  
CURRENT FILING DATE: 2002-10-15  
PRIOR APPLICATION NUMBER: 09/687,483

```

; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/217,658
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/159,176
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/663,968
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-272-665-109
```

```

Query Match      64.8%; Score 16.2; DB 15; Length 100;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 GGGCGCCAACTGCTAGGAT 22
      |||||
Db      64 GGGCGTCAACTGCAAGTAT 84
```

```

RESULT 11
US-10-273-321-108
; Sequence 108, Application US/10273321
; Publication No. US20030180749A1
; GENERAL INFORMATION:
; APPLICANT: Braun et al.
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
; FILE REFERENCE: 24736-2033B
; CURRENT FILING DATE: 2002-10-15
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/687,483
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/217,658
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/159,176
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/663,968
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-273-321-108
```

```

Query Match      64.8%; Score 16.2; DB 15; Length 100;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 GGGCGCCAACTGCTAGGAT 22
      |||||
Db      64 GGGCGTCAACTGCAAGTAT 84
```

```

RESULT 12
US-10-273-321-109
; Sequence 109, Application US/10273321
; Publication No. US20030180749A1
; GENERAL INFORMATION:
; APPLICANT: Braun et al.
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
; FILE REFERENCE: 24736-2033B
```

```

; CURRENT APPLICATION NUMBER: US/10/273,321
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 09/687,483
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/217,658
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/159,176
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/663,968
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-273-321-109
```

```

Query Match      64.8%; Score 16.2; DB 15; Length 100;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 GGGCGCCAACTGCTAGGAT 22
      |||||
Db      64 GGGCGTCAACTGCAAGTAT 84
```

```

RESULT 13
US-10-272-756-108
; Sequence 108, Application US/10272756
; Publication No. US20030190644A1
; GENERAL INFORMATION:
; APPLICANT: Braun et al.
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
; FILE REFERENCE: 24736-2033C
; CURRENT FILING DATE: 2002-10-15
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/687,483
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/217,658
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/159,176
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/663,968
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-272-756-108
```

```

Query Match      64.8%; Score 16.2; DB 15; Length 100;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 GGGCGCCAACTGCTAGGAT 22
      |||||
Db      64 GGGCGTCAACTGCAAGTAT 84
```

```

RESULT 14
US-10-272-756-109
; Sequence 109, Application US/10272756
; Publication No. US20030190644A1
; GENERAL INFORMATION:
; APPLICANT: Braun et al.
```



```

; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
; FILE REFERENCE: 24736-2033C
; CURRENT APPLICATION NUMBER: US/10/272,756
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 09/687,483
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/217,658
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/159,176
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/663,968
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-272-756-109
```

```

Query Match          64.8%; Score 16.2; DB 15; Length 100;
Best Local Similarity 85.7%; Pred.No.3,1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      2 GGGGCGCAACCTGCTAGGAT 22
      |||||
Db      64 GGGGCTCAACCTGCAAGSTAT 84
```

```

RESULT 15
US-10-273-228-108
; Sequence 108, Application US/10273228
; Publication No. US20030207297A1
; GENERAL INFORMATION:
; APPLICANT: Braun et al.
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
; FILE REFERENCE: 24736-2033D
; CURRENT APPLICATION NUMBER: US/10/273,228
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 09/687,483
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/217,658
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/159,176
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/663,968
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-273-228-108
```

```

Query Match          64.8%; Score 16.2; DB 16; Length 100;
Best Local Similarity 85.7%; Pred.No.3,1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      2 GGGGCGCAACCTGCTAGGAT 22
      |||||
Db      64 GGGGCTCAACCTGCAAGSTAT 84
```

Search completed: August 31, 2004, 06:17:02  
Job time : 1823.08 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 00:20:52 / Search time 1095.38 Seconds

(without alignments)  
2057.592 Million cell updates/sec

Title: US-10-001-407-15

Perfect score: 52

Sequence: 1 aacttaatacgaactcactat.....gccaaactgctaggatttc 52

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 1846492

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_ba:\*

2: gb\_hcg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_scs:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

15: em\_da:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_ph:\*

24: em\_pl:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_scs:\*

28: em\_un:\*

29: em\_vi:\*

30: em\_hcg\_hum:\*

31: em\_hcg\_inv:\*

32: em\_hcg\_other:\*

33: em\_hcg\_mus:\*

34: em\_hcg\_pln:\*

35: em\_hcg\_rtd:\*

36: em\_hcg\_mam:\*

37: em\_hcg\_vrc:\*

38: em\_sy:\*

39: em\_hcgo\_hum:\*

40: em\_hcgo\_mus:\*

41: em\_hcgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	52	6	AX498427
2	36.4	70.0	50	6	AR400936
3	36.4	70.0	50	6	AX074095
4	36.4	70.0	50	6	AX498429
5	36.4	70.0	51	6	AR400954
6	36.4	70.0	51	6	AX074113
7	36	69.2	54	6	E61328
8	36	69.2	54	6	AR352014
9	31.8	61.2	52	6	AR344818
10	31.8	61.2	52	6	AX397773
11	31.4	60.4	49	6	BD236963
12	31.4	60.4	49	6	AR307449
13	31.4	60.4	52	6	AX025599
14	31.2	60.0	47	6	A99135
15	31.2	60.0	47	6	BD080307
16	30.4	58.5	52	6	E61341
17	30.4	58.5	52	6	AR352027
18	30.2	58.1	50	6	AR344816
19	30.2	58.1	50	6	AX397771
20	30.2	58.1	53	6	AR344848
21	30.2	58.1	53	6	AX397803
22	29.8	57.3	48	6	AR210629
23	29.8	57.3	48	6	AR232027
24	29.8	57.3	48	6	AR399645
25	29.8	57.3	48	6	AX391328
26	29.6	56.9	47	6	AR070666
27	29.6	56.9	47	6	AR157485
28	29.6	56.9	47	6	BD243351
29	29.6	56.9	47	6	I25930
30	29.6	56.9	47	6	BD132855
31	29.4	56.5	51	6	AX708731
32	29.2	56.2	45	6	E61325
33	29.2	56.2	45	6	AR352051
34	29.2	56.2	47	6	AX721018
35	29.2	56.2	53	6	AX802772
36	29.2	56.2	53	6	AX803190
37	28.8	55.4	48	6	AR400952
38	28.8	55.4	48	6	AX074111
39	28.8	55.4	49	6	AR400956
40	28.8	55.4	49	6	AX074115
41	28.8	55.4	50	6	AR344819
42	28.8	55.4	50	6	AX397774
43	28.8	55.4	53	6	I40641
44	28.8	55.4	53	6	I40642
45	28.8	55.4	53	6	I40643

#### ALIGNMENTS

RESULT 1

AX498427

LOCUS

DEFINITION Sequence 15 from Patent WO0234951.

ACCESSION AX498427

VERSION AX498427.1 GI:23343305

KEYWORDS

SOURCE

ORGANISM

synthetic construct

artificial sequences.

REFERENCE

1 Yang, Y.Y. and Burrell, T.A.

AUTHORS

TITLE

Compositions and methods for detecting human immunodeficiency virus

2 (hiv-2)

JOURNAL

Patent: WO 0234951-A 15 02-MAY-2002;

```
Gen-Probe Incorporated (US)
Location/Qualifiers
1..52
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="T7 promoter primer having a promoter sequence
appended at the 5' end of an HIV-2 complementary primer
sequence"

ORIGIN
Query Match 100.0%; Score 52; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 8.6e-10;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTTAATGACCTCACTATAGGAGACGGCGCCCACTGCTAGGATTTT 52
1 AATTTAATGACCTCACTATAGGAGACGGCGCCCACTGCTAGGATTTT 52
Db 1 AATTTAATGACCTCACTATAGGAGACGGCGCCCACTGCTAGGATTTT 52

RESULT 2
AR400936
LOCUS AR400936 50 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 8 from patent US 6623920.
ACCESSION AR400936
VERSION AR400936.1 GI:40148228
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 50)
AUTHORS Bee,G.G., Yang,Y.Y., Kolk,D., Giachetti,C. and McDonough,S.H.
TITLES Detection of HIV-1 by nucleic acid amplification
JOURNAL Patent: US 6623920-A 8 23-SEP-2003;
FEATURES
Location/Qualifiers
1..50
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 70.0%; Score 36.4; DB 6; Length 50;
Best Local Similarity 94.2%; Pred. No. 0.0016;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 AATTTAATGACCTCACTATAGGAGACGGCGCCCACTGCTAGGATTTT 52
1 AATTTAATGACCTCACTATAGGAGACGGCGCCCACTGCTAGGATTTT 52
Db 1 AATTTAATGACCTCACTATAGGAGACGGCGCCCACTGCTAGGATTTT 50

RESULT 3
AX074095
LOCUS AX074095 50 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 8 from Patent WO0104361.
ACCESSION AX074095
VERSION AX074095.1 GI:12710307
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE artificial sequences.
1
AUTHORS Bee,G.G., Yang,Y.Y., Kolk,D.P., Giachetti,C. and McDonough,S.H.
TITLES Detection of HIV-1 by nucleic acid amplification
JOURNAL Patent: WO 0104361-A 8 18-JAN-2001;
Gen-Probe Incorporated (US) ; Bee, Gary G. (US) ; Yang, Yeasing Y.
(US) ; Kolk, Dan P. (US) ; Giachetti, Cristina (US) ; McDonough,
Sherrol Hoffa (US)
FEATURES
Location/Qualifiers
1..50
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="synthetic amplification oligomer with 5' promoter
sequence, for HIV-1 LTR region"

Gen-Probe Incorporated (US)
Location/Qualifiers
1..52
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="T7 promoter primer having a promoter sequence
appended at the 5' end of an HIV-2 complementary primer
sequence"

ORIGIN
Query Match 100.0%; Score 52; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 8.6e-10;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTTAATGACCTCACTATAGGAGACGGCGCCCACTGCTAGGATTTT 52
1 AATTTAATGACCTCACTATAGGAGACGGCGCCCACTGCTAGGATTTT 52
Db 1 AATTTAATGACCTCACTATAGGAGACGGCGCCCACTGCTAGGATTTT 52

RESULT 4
AX498429
LOCUS AX498429 50 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 17 from Patent WO0234951.
ACCESSION AX498429
VERSION AX498429.1 GI:23343307
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE artificial sequences.
1
AUTHORS Yang,Y.Y. and Burrell,T.A.
TITLES Compositions and methods for detecting human immunodeficiency virus
JOURNAL Patent: WO 0234951-A 17 02-MAY-2002;
Gen-Probe Incorporated (US)
FEATURES
Location/Qualifiers
1..50
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="T7 promoter primer having a promoter sequence
appended at the 5' end of the sequence given as SEQ ID
NO:12"

ORIGIN
Query Match 70.0%; Score 36.4; DB 6; Length 50;
Best Local Similarity 94.2%; Pred. No. 0.0016;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 AATTTAATGACCTCACTATAGGAGACGGCGCCCACTGCTAGGATTTT 52
1 AATTTAATGACCTCACTATAGGAGACGGCGCCCACTGCTAGGATTTT 52
Db 1 AATTTAATGACCTCACTATAGGAGACGGCGCCCACTGCTAGGATTTT 50

RESULT 5
AR400954
LOCUS AR400954 51 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 26 from patent US 6623920.
ACCESSION AR400954
VERSION AR400954.1 GI:40148246
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 51)
AUTHORS Bee,G.G., Yang,Y.Y., Kolk,D., Giachetti,C. and McDonough,S.H.
TITLES Detection of HIV-1 by nucleic acid amplification
JOURNAL Patent: US 6623920-A 26 23-SEP-2003;
Gen-Probe Incorporated (US) ; Bee, Gary G. (US) ; Yang, Yeasing Y.
(US) ; Kolk, Dan P. (US) ; Giachetti, Cristina (US) ; McDonough,
Sherrol Hoffa (US)
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"

ORIGIN
Query Match 70.0%; Score 36.4; DB 6; Length 51;
Best Local Similarity 94.2%; Pred. No. 0.0016;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 AATTTAATGACCTCACTATAGGAGACGGCGCCCACTGCTAGGATTTT 52
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Db 1 AATTTAATGACCTCACTATAGGAGACGGCGCCCACTGCTAGGATTTT 50
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RESULT 6  
LOCUS AX074113 51 bp DNA linear PAT 06-FEB-2001  
DEFINITION Sequence 26 from Patent WO0104361.  
ACCESSION AX074113  
VERSION AX074113.1 GI:12710325  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Bee,G., Yang,Y.Y., Kolk,D.P., Giachetti,C. and McDonough,S.H.  
TITLE Detection of hiv-1 by nucleic acid amplification  
JOURNAL Patent: WO 0104361-A 26 18-JUN-2001;  
Gen-Probe Incorporated (US) ; Bee, Gary G. (US) ; Yang, Yeasing Y.  
(US) ; Kolk, Dan P. (US) ; Giachetti, Cristina (US) ; McDonough,  
Sherrol Hoffa (US)  
FEATURES  
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ORIGIN  
Query Match 70.0%; Score 36.4; DB 6; Length 51;  
Best Local Similarity 94.2%; Pred. No. 0.0016;  
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;  
Oy 1 AATTATACGACTACTATAGGAGACGGCGCCCACTGCTAGGATTT 52  
1 AATTATACGACTACTATAGGAGACGGCGCCCACTGCTAGGATTT 50  
Db 1 AATTATACGACTACTATAGGAGACGGCGCCCACTGCTAGGATTT 50

RESULT 7  
LOCUS E61328 54 bp DNA linear PAT 18-JUN-2001  
DEFINITION Probe for detecting oligonucleotide.  
ACCESSION E61328  
VERSION E61328.1 GI:13025890  
KEYWORDS JP 199046778-A/2.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 54)  
AUTHORS Daniel,L.K. and Timothy,J.F.  
TITLE Probe for detecting oligonucleotide  
JOURNAL Patent: JP 199046778-A 2 23-FEB-1999;  
GEN-PROB INC  
COMMENT OS Artificial Sequence  
PN JP 199046778-A/2  
PD 23-FEB-1999  
PF 14-JAN-1998 JP 1998005607  
PR 11-JUL-1989 US 379501  
PI DANIEL LOUIS KASHIAN,TIMOTHY J FURUTSU  
PC C12N15/09,C12Q1/68,C12N15/00  
CC  
FH Key Location/Qualifiers  
FT source 1..54  
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1..54  
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1 AATTATACGACTACTATAGGAGACGGCGCCCACTGCTAGGATTT 52  
Db 1 AATTATACGACTACTATAGGAGACGGCGCCCACTGCTAGGATTT 52

RESULT 8  
LOCUS AR352014 54 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 2 from patent US 6589734.  
ACCESSION AR352014  
VERSION AR352014.1 GI:33756977  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 54)  
AUTHORS Kacian,D.L., Fultz,T.J. and McDonough,S.H.  
TITLE Detection of HIV  
JOURNAL Patent: US 6589734-A 2 08-JUL-2003;  
Location/Qualifiers  
1..54  
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/mol\_type="genomic DNA"

ORIGIN  
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Best Local Similarity 80.8%; Pred. No. 0.0023;  
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Oy 1 AATTATACGACTACTATAGGAGACGGCGCCCACTGCTAGGATTT 52  
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RESULT 9  
LOCUS AR344818 52 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 7 from patent US 6582920.  
ACCESSION AR344818  
VERSION AR344818.1 GI:33740899  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 52)  
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.  
TITLE Amplification of HIV-1 RT sequences for detection of sequences  
associated with drug-resistance mutations  
JOURNAL Patent: US 6582920-A 7 24-JUN-2003;  
Location/Qualifiers  
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Best Local Similarity 76.5%; Pred. No. 0.11;  
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Db 1 AATTATACGACTACTATAGGAGACGGCGCCCACTGCTAGGATTT 51

RESULT 10  
LOCUS AX397773 52 bp DNA linear PAT 27-MAY-2002  
DEFINITION Sequence 7 from Patent WO0220852.  
ACCESSION AX397773  
VERSION AX397773.1 GI:21260647  
KEYWORDS  
SOURCE synthetic construct

ORGANISM synthetic construct  
artificial sequences.

REFERENCE  
1 Yang, Y., Brenbano, S.T., Babola, O., Tran, N. and Vernet, G.  
Amplification of hiv-1 sequences for detection of sequences  
associated with drug-resistance mutations  
Patent: WO 020852-A 7 14-MAR-2002;  
Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)

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promoter  
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Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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1 AATTATACGACTCATTAGGAGACCGACCATCATTCATTCCTGCTT 51

Db 1 AATTATACGACTCATTAGGAGACCGACCATCATTCATTCCTGCTT 51

RESULT 11  
BD236963 49 bp DNA linear PAT 17-JUL-2003  
LOCUS BD236963  
DEFINITION Nucleic acid sequence for detecting genetic marker for cancer in  
biological samples.  
ACCESSION BD236963.1 GI:33046733  
VERSION JP 2002535014-A/38.  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 49)  
HARVEY, R.C. and CLARK, T.J.C.  
Nucleic acid sequence for detecting genetic marker for cancer in  
biological samples  
Patent: JP 2002535014-A 38 22-OCT-2002;  
JOURNAL GEN PROBE INC  
COMMENT OS Artificial Sequence  
PN JP 2002535014-A/38  
PF 28-JAN-2000 JP 2000596180  
PR 28-JAN-1999 US 60/117640  
PI RICHARD C HARVEY, THOMAS J CLARK JR  
PC C12N15/09, C1201/68, C12N15/00  
CC Description of Artificial Sequence: synthetic construct FH  
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1 AATTATACGACTCATTAGGAGACGGCGCCCACTG 41  
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1 AATTATACGACTCATTAGGAGACGGCGCCCACTG 41

Db 2 AATTATACGACTCATTAGGAGACGTGCTGACCTG 42

RESULT 12  
AR307449 49 bp DNA linear PAT 12-JUN-2003  
LOCUS AR307449

DEFINITION Sequence 38 from patent US 6551778.  
ACCESSION AR307449  
VERSION AR307449.1 GI:31697988  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 49)  
HARVEY, R.C. and CLARK, T.J. Jr.  
Nucleic acid sequences for detecting genetic markers for cancer in  
a biological sample  
Patent: US 6551778-A 38 22-APR-2003;  
JOURNAL Location/Qualifiers  
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1. .49  
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ORIGIN  
1 AATTATACGACTCATTAGGAGACGGCGCCCACTG 41  
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Db 2 AATTATACGACTCATTAGGAGACGTGCTGACCTG 42

RESULT 13  
AX025599 52 bp DNA linear PAT 16-SEP-2000  
LOCUS AX025599  
DEFINITION Sequence 78 from Patent WO0034517.  
ACCESSION AX025599  
VERSION AX025599.1 GI:10187267  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
Tan, P.S., van Maanen, C., Wagter, L.H., Schut, F., Brinkhof, J.M.,  
Eising, H.Z., and Koopmans, H.H.  
Detection of mycobacterium avium subspecies  
Patent: WO 0034517-A 78 15-JUN-2000;  
JOURNAL GEZONDHEIDSDIENST VOOR DIEREN (NL) ; MAANEN CORNELIS VAN (NL) ; TAN  
PARIS SOM TUWAN (NL) ; WAGTER LOUAS HENDRIK ALBERT (NL) ;  
MICROSCHEEN B V (NL) ; SCHUT FREDERIK (NL) ; BRINKHOF JOHANNES  
MICHEL ANTH (NL) ; EISING HENRIETTE ZWAANTJINA (NL) ; KOOPMANS  
HENDRIK HIDDO (NL)

FEATURES  
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Location/Qualifiers  
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1 AATTATACGACTCATTAGGAGACGGCGCCCACTG 41  
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Qy 1 AATTATACGACTCATTAGGAGACGGCGCCCACTG 41  
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Db 2 AATTATACGACTCATTAGGAGACGTGCTGACCTG 42

RESULT 14  
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LOCUS A99135  
DEFINITION Sequence 9 from Patent WO907898.  
ACCESSION A99135  
VERSION A99135.1 GI:6782088  
KEYWORDS unidentified  
SOURCE unidentified  
ORGANISM unidentified



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 00:19:57 ; Search time 343.065 Seconds

(without alignments)  
643.920 Million cell updates/sec

Title: US-10-001-407-15

Perfect score: 52  
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Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 3485926

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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3: geneeqn2000s:\*  
4: geneeqn2001as:\*  
5: geneeqn2001bs:\*  
6: geneeqn2002s:\*  
7: geneeqn2003as:\*  
8: geneeqn2003bs:\*  
9: geneeqn2003cs:\*  
10: geneeqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	52	6	ABK93891 Human imm
2	36.4	70.0	50	6	AAAF56540 HIV-1 det
3	36.4	70.0	50	6	ABK93893 Human imm
4	36.4	70.0	51	5	AAAF56558 HIV-1 det
5	36	69.2	53	2	AAV66330 Human imm
6	36	69.2	54	2	AAQ86607 Human imm
7	36	69.2	54	2	AAAT15552 Human imm
8	36	69.2	54	2	AAAX23172 HIV regio
9	36	69.2	52	6	AAAD62557 HIV-1 pro
10	31.8	61.2	52	6	ABK53107 HIV-1 pro
11	31.8	61.2	52	6	AAI45469 HIV-1 pro
12	31.4	60.4	49	3	AAAT76206 Human pro
13	31.4	60.4	52	3	AAAF63315 Mycobacte
14	31.2	60.0	47	2	AAAX26214 Oligo com
15	31.2	60.0	47	9	AADE48105 PCR prime
16	31.2	59.6	48	2	AAQ56491 PCR prime
17	31	59.6	48	2	AAAT91790 Human BB
18	30.4	58.5	52	2	AAQ86620 Human imm
19	30.4	58.5	52	2	AAQ86639 Modified
20	30.4	58.5	52	2	AAAT15575 Multiple
21	30.4	58.5	52	2	AAAT15565 Human imm
22	30.4	58.5	52	2	AAAT42408 HIV probe
23	30.4	58.5	52	2	AAV66343 Human imm

24	30.4	58.5	52	2	AAV66357 CML-2 chr
25	30.4	58.5	52	2	AAAX23208 CML t(14;
26	30.4	58.5	52	2	AAAX23185 HIV regio
27	30.4	58.5	52	2	AAAD62570 Human imm
28	30.2	58.1	50	6	ABK53105 HIV-1 gag
29	30.2	58.1	50	6	AAI45467 HIV-1 gag
30	30.2	58.1	53	6	ABK53137 HIV-1 pro
31	30.2	58.1	53	6	AAI45499 HIV-1 pro
32	29.8	57.3	48	2	AAAT3689 Human pri
33	29.8	57.3	48	2	AAAC58539 Human DNA
34	29.8	57.3	48	3	AAAT7716 Human PRO
35	29.8	57.3	48	4	AAAC97508 Human PRO
36	29.8	57.3	48	4	AAAC93118 Human PRO
37	29.8	57.3	48	7	ABBS57299 Promoter-1
38	29.6	56.9	47	2	AAQ50478 Promoter-
39	29.6	56.9	47	2	AAQ57043 M. tuberc
40	29.6	56.9	47	2	AAAX57024 WO923258
41	29.6	56.9	47	3	AAAB89903 Amplifica
42	29.6	56.9	52	8	AAAC43281 Nucleotid
43	29.4	56.5	47	2	AAAT91784 Primer BB
44	29.4	56.5	51	6	ABT12953 Mycobacte
45	29.2	56.2	45	2	AAQ86640 Promoter-

#### ALIGNMENTS

RESULT 1  
ID ABK93891 standard; DNA; 52 BP.  
XX  
AC ABK93891;  
XX  
DT 29-AUG-2003 (revised)  
DT 26-AUG-2002 (first entry)  
XX  
DE Human immunodeficiency virus type 2 detection probe #15.  
XX  
KW Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;  
KW hepatitis C virus; HCV; probe; ss.  
XX  
OS Human immunodeficiency virus 2.  
XX  
PN WO200234951-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 22-OCT-2001; 2001WO-US045396.  
XX  
PR 23-OCT-2000; 2000US-0242620P.  
PR 30-MAR-2001; 2001US-0280058P.  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Yang YV, Burrell TA;  
XX  
DR WPI; 2002-489953/52.  
XX  
PT Detecting human immunodeficiency virus-2 nucleic acids in a sample, by  
PT amplifying nucleic acids with oligonucleotides and detecting nucleic  
PT acid, or hybridizing nucleic acid with a probe and detecting probe:target  
PT duplex.  
XX  
PS Claim 11; Page 25; 58pp; English.  
XX  
CC The invention relates to a method of detecting human immunodeficiency  
CC virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with  
CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide  
CC base sequence, and detecting the amplified NA; or providing a  
CC hybridisation probe and detectable label, hybridising HIV-2 NA with the  
CC probe to form probe:target duplex, and detecting the duplex. The method  
CC is useful for detecting the presence of HIV-2 NAs in a lysate or a blood  
CC product such as plasma or serum, and also for detecting subtypes A, B, C

CC and D of HIV-2. The method is useful for amplifying and detecting the NA  
 CC in blood serum and also as components of multiplex amplification  
 CC reactions that synthesize amplicons corresponding to polynucleotides of  
 CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C  
 CC virus (HCV). ABR3877-ABR3910 represent HIV-2 detection probes of the  
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 52 BP; 15 A; 11 C; 13 G; 13 T; 0 U; 0 Other;

## Query Match

Best Local Similarity 100.0%; Score 52; DB 6; Length 52;  
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTAATACGACTCCTATAGGAGACGGGCGCACTGCTAGGATTTT 52  
 DB 1 AATTAATACGACTCCTATAGGAGACGGGCGCACTGCTAGGATTTT 52

## RESULT 2

AAFS6540  
 ID AAF56540 standard; DNA; 50 BP.

AC AAF56540;

DT 11-SEP-2003 (revised)

DT 18-APR-2001 (first entry)

DE HIV-1 detection PCR primer SEQ ID NO: 8.

KW HIV-1 detection; diagnosis; blood screening; PCR primer; probe; ss.

OS Human immunodeficiency virus 1.

PN MO200104361-A2.

PD 18-JUN-2001.

PF 07-JUL-2000; 2000MO-US018665.

PR 09-JUL-1999; 99US-0143072P.

PA (GENP-) GEN-PROBE INC.

PA (BERG/) BEB G.G.

PA (YANG/) YANG Y.Y.

PA (KOLK/) KOLK D.P.

PA (GIAC/) GIACCHETTI C.

PA (MCDO/) MCDONOUGH S.H.

PI Bee CG, Yang Y, Kolk DP, Giachetti C, McDonough SH;

DR WPI; 2001-147200/15.

PT Detecting HIV-1 nucleic acids in biological samples useful for diagnosing  
 PT HIV-1 infection involves using nucleic acid capture oligomers,  
 PT amplification oligomers and probe oligomers.

PS Claim 5; Page 50; 60pp; English.

CC The present invention provides probes and PCR primers for use in the  
 CC detection of HIV-1. These are shown in AAF56533-AAF56589. They can be  
 CC used to diagnose HIV infection and to ensure that blood and blood  
 CC products do not contain the virus, thus enabling the prevention of HIV  
 CC infection during blood transfusions. (Updated on 11-SEP-2003 to  
 CC standardise OS field)

XX Sequence 50 BP; 15 A; 10 C; 12 G; 13 T; 0 U; 0 Other;

## Query Match

Best Local Similarity 70.0%; Score 36.4; DB 5; Length 50;  
 Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 AATTAATACGACTCCTATAGGAGACGGGCGCACTGCTAGGATTTT 52  
 ID AATTAATACGACTCCTATAGGAGACGGGCGCACTGCTAGGATTTT 52

DB 1 AATTAATACGACTCCTATAGGAGACGGGCGCA--CTGCTAGGATTTT 50

## RESULT 3

ABR3893  
 ID ABR3893 standard; DNA; 50 BP.

AC ABR3893;

DT 29-AUG-2003 (revised)

DT 26-AUG-2002 (first entry)

DE Human immunodeficiency virus type 2 detection probe #17.

KW Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;  
 KW hepatitis C virus; HCV; probe; ss.

OS Human immunodeficiency virus 2.

PN MO200234951-A2.

PD 02-MAY-2002.

PF 22-OCT-2001; 2001MO-US045396.

PR 23-OCT-2000; 2000US-0242620P.

PR 30-MAR-2001; 2001US-0280058P.

PA (GENP-) GEN-PROBE INC.

PI Yang Y, Burrell TA;

DR WPI; 2002-489953/52.

PT Detecting human immunodeficiency virus-2 nucleic acids in a sample, by  
 PT amplifying nucleic acids with oligonucleotides and detecting nucleic  
 PT acid, or hybridizing nucleic acid with a probe and detecting probe:target  
 PT duplex.

PS Claim 11; Page 25; 58pp; English.

CC The invention relates to a method of detecting human immunodeficiency  
 CC virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with  
 CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide  
 CC base sequence, and detecting the amplified NA; or providing a  
 CC hybridisation probe and detectable label, hybridising HIV-2 NA with the  
 CC probe to form probe:target duplex, and detecting the duplex. The method  
 CC is useful for detecting the presence of HIV-2 NA in a lysate or a blood  
 CC product such as plasma or serum, and also for detecting subtypes A, B, C  
 CC and D of HIV-2. The method is useful for amplifying and detecting the NA  
 CC reactions that synthesize amplicons corresponding to polynucleotides of  
 CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C  
 CC virus (HCV). ABR3877-ABR3910 represent HIV-2 detection probes of the  
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 50 BP; 15 A; 10 C; 12 G; 13 T; 0 U; 0 Other;

## Query Match

Best Local Similarity 70.0%; Score 36.4; DB 6; Length 50;  
 Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 AATTAATACGACTCCTATAGGAGACGGGCGCACTGCTAGGATTTT 52  
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## RESULT 4

AAFS6558  
 ID AAF56558 standard; DNA; 51 BP.

AC AAF56558;

DT 11-SEP-2003 (revised)  
 DT 18-APR-2001 (first entry)  
 XX  
 DE HIV-1 detection PCR primer SEQ ID NO: 26.  
 XX  
 KM HIV-1 detection; diagnosis; blood screening; PCR primer; probe; ss.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN W0200104361-A2.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 07-JUL-2000; 2000WO-US018685.  
 XX  
 PR 09-JUL-1999; 99US-0143072P.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 PA (BEEG/) BEE G G.  
 PA (YANG/) YANG Y Y.  
 PA (KOLK/) KOLK D P.  
 PA (GIAC/) GIACHETTI C.  
 PA (MCDON/) MCDONOUGH S H.  
 PI Bee GG, Yang YV, Kolk DP, Giachetti C, McDonough SH;  
 XX WPI; 2001-147200/15.  
 DR  
 PT Detecting HIV-1 nucleic acids in biological samples useful for diagnosing  
 PT HIV-1 infection involves using nucleic acid capture oligomers,  
 PT amplification oligomers and probe oligomers.  
 XX  
 PS Claim 5; Page 54; 60pp; English.  
 XX  
 CC The present invention provides probes and PCR primers for use in the  
 CC detection of HIV-1. These are shown in AAF56533-AAF56589. They can be  
 CC used to diagnose HIV infection and to ensure that blood and blood  
 CC products do not contain the virus, thus enabling the prevention of HIV  
 CC infection during blood transfusions. (Updated on 11-SEP-2003 to  
 CC standardise OS field)  
 CC  
 SQ Sequence 51 BP; 15 A; 11 C; 12 G; 13 T; 0 U; 0 Other;  
 XX  
 Query Match 70.0%; Score 36.4; DB 5; Length 51;  
 Best Local Similarity 94.2%; Pred. No. 8.6e-06;  
 Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;  
 QY 1 AATTATAGAGCTGACTATAGGAGACGGGCGCCCACTGCTAGGATTTT 52  
 1 AATTATAGAGCTGACTATAGGAGACGGGCGCCCACTGCTAGGATTTT 50  
 DB  
 RESULT 5  
 AAV6330  
 ID AAV6330 standard; DNA; 53 BP.  
 XX  
 AC AAV6330;  
 XX  
 DT 06-JAN-1999 (first entry)  
 XX  
 DE Human immunodeficiency virus region 1 (+) primer.  
 XX  
 KM Region 1; block splice template; autocatalytic RNA amplification; primer;  
 KM ss.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus.  
 XX  
 PN US5824518-A.  
 XX  
 PD 20-OCT-1998.  
 XX  
 PF 06-JUN-1995; 95US-00469067.

XX  
 PR 11-JUL-1989; 89US-00379501.  
 PR 10-JUL-1990; 90US-00550837.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Fultz TJ, Kacian DL;  
 XX WPI; 1998-58257/49.  
 DR  
 PT Block splice template useful for amplification of nucleic acids -  
 PT comprises two nucleic acid regions, the first region located 3' of the  
 PT second region and blocked at its 3' terminus to inhibit primer extension  
 PT by a DNA polymerase.  
 XX  
 PS Disclosure; Col 9; 51pp; English.  
 XX  
 CC AAV6330-31 represent Human immunodeficiency virus region 1 primers. The  
 CC primers are used to exemplify the invention, together with probe  
 CC AAV6332. The specification describes methods of synthesising multiple  
 CC copies of a target nucleic acid sequence autocatalytically under  
 CC conditions of substantially constant temperature, ionic strength and pH  
 CC are provided in which multiple RNA copies of the target sequence  
 CC autocatalytically generate additional copies. The target sequence is a  
 CC block splice template which comprises two nucleic acid regions. The first  
 CC region is located 3' of the second region and is blocked at its 3'  
 CC terminus to inhibit primer extension by a DNA polymerase, and the second  
 CC region comprises a promoter sequence recognised by an RNA polymerase. The  
 CC methods are used to amplify nucleic acids, especially RNA, for analysis,  
 CC cloning or probe production  
 XX  
 SQ Sequence 53 BP; 15 A; 11 C; 13 G; 14 T; 0 U; 0 Other;  
 XX  
 Query Match 69.2%; Score 36; DB 2; Length 53;  
 Best Local Similarity 80.8%; Pred. No. 1.3e-05;  
 Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 AATTATAGAGCTGACTATAGGAGACGGGCGCCCACTGCTAGGATTTT 52  
 1 AATTATAGAGCTGACTATAGGAGACGGGCGCCCACTTCCGTGGGACTTT 52  
 DB  
 RESULT 6  
 AAQ86607  
 ID AAQ86607 standard; DNA; 54 BP.  
 XX  
 AC AAQ86607;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 15-NOV-1995 (first entry)  
 XX  
 DE Human immunodeficiency virus (HIV) region 1 plus strand primer.  
 XX  
 KM Primer; autocatalytic; target; HIV; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5399491-A.  
 XX  
 PD 21-MAR-1995.  
 XX  
 PF 19-MAR-1992; 92US-00855732.  
 XX  
 PR 11-JUL-1989; 89US-00379501.  
 PR 10-JUL-1990; 90US-00550837.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Fultz TJ, Kacian DL;  
 XX WPI; 1995-130686/17.  
 DR  
 PT Amplification of nucleic acid targets - using a reverse transcriptase

PT with RNase H activity and a RNA polymerase at constant temp.  
 XX  
 PS Disclosure; Col 9; 58pp; English.  
 XX

CC AA086607-09 are primers and a probe for the human immunodeficiency virus  
 CC region 1. They are used to produce autocatalytic oligonucleotides which  
 CC require no change in the experimental conditions i.e. constant  
 CC temperature, pH and ionic strength. These sequences are useful in  
 CC generating multiple copies of specific nucleic acid target sequences.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX

SO Sequence 54 BP; 15 A; 12 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 69.2%; Score 36; DB 2; Length 54;  
 Best Local Similarity 80.8%; Pred. No. 1.3e-05;  
 Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 AATTTAATACGACTCTATAGGAGACGGGCGCAACTGCTAGGATTTT 52  
 1 AATTTAATACGACTCTATAGGAGACGAGGACTTCCGCTGGGACTTT 52  
 DB

# RESULT 7

AAT15552  
 ID AAT15552 standard; DNA; 54 BP.  
 XX  
 AC AAT15552;  
 XX

DT 25-MAR-2003 (revised)  
 DT 16-JUL-1996 (first entry)  
 XX

DE Human immunodeficiency virus (HIV) region 1 (+) primer.  
 XX

KW Human immunodeficiency virus; HIV; region 1; primer; auto-catalytic;  
 KW synthesis; RNA target sequence; assay; detection; quantification; ss.  
 XX  
 OS Synthetic.  
 XX

PN US5480784-A.  
 XX

PD 02-JAN-1996.  
 XX

PF 10-JUL-1990; 90US-00550837.  
 XX

PR 11-JUL-1989; 89US-00379501.  
 XX

PA (GENP-) GEN-PROBE INC.  
 XX

PI Fultz TJ, Kacian DJ;  
 XX

PS WPI; 1996-068248/07.  
 XX

PT Auto-catalytic synthesis of multiple copies of an RNA target sequence -  
 PT use cooperative action of a DNA and RNA polymerase in presence of RNase  
 PT H, useful for detection of target sequence e.g. in clinical or  
 PT environmental sample.  
 XX

PS Example; Col 9-10; 51pp; English.  
 XX

CC The present sequence is a primer for the human immunodeficiency virus  
 CC region 1, which was used to demonstrate an improved method for  
 CC synthesizing multiple copies of a RNA target sequence. The method  
 CC comprises combining the target with a primer which hybridizes to the 3'-  
 CC terminal portion of the target, a promoter primer which hybridizes with a  
 CC and/or quantitate specific target sequences in clinical, environmental or  
 CC forensic samples. It can be used as a component of an assay to detect  
 CC using the cooperative action of a DNA polymerase, e.g. a reverse  
 CC transcriptase and avoids repetitive manipulations of reaction conditions,  
 CC e.g. temp., ionic strength and pH. (Updated on 25-MAR-2003 to correct PF  
 CC field.)  
 XX

SO Sequence 54 BP; 15 A; 12 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 69.2%; Score 36; DB 2; Length 54;  
 Best Local Similarity 80.8%; Pred. No. 1.3e-05;  
 Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 AATTTAATACGACTCTATAGGAGACGGGCGCAACTGCTAGGATTTT 52  
 1 AATTTAATACGACTCTATAGGAGACGAGGACTTCCGCTGGGACTTT 52  
 DB

# RESULT 8

AAX23172  
 ID AAX23172 standard; DNA; 54 BP.  
 XX  
 AC AAX23172;  
 XX

DT 11-JUN-1999 (first entry)  
 DT XX  
 DE HIV region 1 primer #1.  
 XX

KW Autocatalytic amplification; transcription-based amplification;  
 KW thermal cycling; diagnostic; environmental testing; probe; detection;  
 KW genetic disease; infectious disease; microorganism; food; forensic;  
 KW paternity; primer; ss.  
 XX  
 OS Synthetic.  
 XX

PN US5888779-A.  
 XX

PD 30-MAR-1999.  
 XX

PF 05-JUN-1995; 95US-00461654.  
 XX

PR 11-JUL-1989; 89US-00379501.  
 XX

PR 10-JUL-1990; 90US-00550837.  
 XX

PA (GENP-) GEN-PROBE INC.  
 XX

PI Fultz TJ, Kacian DJ;  
 XX

PS WPI; 1999-253231/21.  
 XX

PT Kit for autocatalytic amplification of RNA targets.  
 PT XX  
 PS Disclosure; Col 9; 51pp; English.  
 XX

CC This invention describes a novel method for the autocatalytic  
 CC amplification of an RNA target in a transcription-based amplification  
 CC system without thermal cycling. The method generates oligonucleotides for  
 CC diagnostic or environmental testing, for use e.g. as probes and in  
 CC cloning. Typical applications are the detection of genetic or infectious  
 CC diseases, the monitoring of responses to therapy, the quantitation or  
 CC detection of microorganisms in foods, forensic studies and the  
 CC establishment of paternity. Kits containing the products of the invention  
 CC provide many copies of selected RNA targets under conditions of constant  
 CC temperature, ionic strength and pH. Specific amplification of RNA targets  
 CC increases sensitivity, convenience, accuracy and the reliability of  
 CC assays  
 XX

SO Sequence 54 BP; 15 A; 12 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 69.2%; Score 36; DB 2; Length 54;  
 Best Local Similarity 80.8%; Pred. No. 1.3e-05;  
 Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 AATTTAATACGACTCTATAGGAGACGGGCGCAACTGCTAGGATTTT 52  
 1 AATTTAATACGACTCTATAGGAGACGAGGACTTCCGCTGGGACTTT 52  
 DB

# RESULT 9

AAD62557  
ID AAD62557 standard; DNA; 54 BP.  
XX  
AC AAD62557;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human immunodeficiency virus (HIV) region 1 specific PCR primer #1.  
XX  
KW Amplification; human immunodeficiency virus; environmental testing; HIV;  
KM detection; diagnostic testing; PCR; primer; ss.  
XX  
OS Human immunodeficiency virus.  
XX  
PN US6589734-B1.  
XX  
PD 08-JUL-2003.  
XX  
PF 08-OCT-1998; 98US-00168947.  
XX  
PR 11-JUL-1989; 89US-00379501.  
PR 10-JUL-1990; 90US-00550837.  
PR 06-JUN-1995; 95US-00469067.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Kacian DL, Fultz TJ, McDonough SH;  
XX  
DR WPI; 2003-810379/76.  
XX  
PT New oligonucleotide probe, useful in detecting HIV nucleic acid in a  
PT sample and for environmental and diagnostic testing.  
XX  
PS Claim 13; Col 9; 62pp; English.  
XX  
CC The invention relates to oligonucleotides useful in amplifying and  
CC detecting human immunodeficiency virus (HIV) nucleic acid in a sample.  
CC The invention is used for environmental testing, diagnostic testing,  
CC research studies and for the preparation of reagents or materials for  
CC cloning or other purposes. The present sequence is HIV region specific  
CC PCR primer. This sequence is used in the invention  
XX  
SQ Sequence 54 BP; 15 A; 12 C; 13 G; 14 T; 0 U; 0 Other;  
XX  
Query Match 69.2%; Score 36; DB 9; Length 54;  
Best Local Similarity 80.8%; Pred. No. 1.3e-05;  
Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
OY 1 AATTATACGACTCATATAGGAGACGGCGCCACCTGCTAGGATTT 52  
DB 1 AATTATACGACTCATATAGGAGACGAGCACTTCCGCGGAGACTTT 52  
RESULT 10  
ABK53107  
ID ABK53107 standard; DNA; 52 BP.  
XX  
AC ABK53107;  
XX  
DT 29-AUG-2003 (revised)  
DT 12-AUG-2002 (first entry)  
XX  
DE HIV-1 protease gene specific oligonucleotide primer #1.  
XX  
KW HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;  
KM reverse transcriptase; infection; PCR.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN US2002055095-A1.  
XX  
PD 09-MAY-2002.  
XX

PF 31-AUG-2001; 2001US-00944036.  
XX  
XX 01-SEP-2000; 2000US-0229790P.  
XX  
XX (YANG/) YANG Y Y.  
PA (BRENT/) BRENTANO S T.  
PA (BABO/) BABOLA O.  
PA (TRAN/) TRAN N.  
PA (VERN/) VERNET G.  
XX  
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;  
XX  
XX WPI; 2002-462902/49.  
XX  
DR  
XX  
PT New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-  
PT 1 and probes for detecting the amplified product are specific for gag and  
PT pol regions and are useful to detect different subtypes of HIV-1.  
XX  
PS Claim 1; Page 14; 37pp; English.  
XX  
CC This invention relates to a series of nucleic acid oligomers for  
CC amplifying and detecting a nucleotide sequence of human immunodeficiency  
CC virus type 1 (HIV-1). The invention also comprises a labeled  
CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived  
CC from gag or pol sequences, having one of the sequences fully defined in  
CC the specification, and a method for detecting HIV-1 in a biological  
CC sample, comprising mixing the sample with two or more of the  
CC amplification oligomers that specifically amplify at least one HIV-1  
CC target sequence within gag and a pol sequence which is a protease or  
CC reverse transcriptase sequence, amplifying the target, and detecting the  
CC amplified product. The oligonucleotides of the invention may be used to  
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer  
CC used to amplify the HIV-1 protease gene in the HIV detection method of  
CC the invention. (Updated on 29-AUG-2003 to standardise OS field)  
XX  
SQ Sequence 52 BP; 16 A; 14 C; 8 G; 14 T; 0 U; 0 Other;  
XX  
Query Match 61.2%; Score 31.8; DB 6; Length 52;  
Best Local Similarity 76.5%; Pred. No. 0.00085;  
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
OY 1 AATTATACGACTCATATAGGAGACGGCGCCACCTGCTAGGATTT 51  
DB 1 AATTATACGACTCATATAGGAGACGACACGCACTCCTCTGCTTT 51  
RESULT 11  
AAL45469  
ID AAL45469 standard; DNA; 52 BP.  
XX  
AC AAL45469;  
XX  
DT 29-AUG-2003 (revised)  
DT 06-JUN-2002 (first entry)  
XX  
DE HIV-1 pol gene protease amplification oligomer SEQ ID NO: 7.  
XX  
KW HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;  
KM probe; ss.  
XX  
OS Human immunodeficiency virus 1.  
OS Enterobacteria phage T7.  
XX  
PN WO200220852-A1.  
XX  
PD 14-MAR-2002.  
XX  
PF 01-SEP-2000; 2000WO-US024117.  
XX  
PR 01-SEP-2000; 2000WO-US024117.  
XX  
PA (GENP-) GEN-PROBE INC.  
PA (INMR) BIOMERIEUX SA.

XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;  
 CC  
 CC  
 DR WPI; 2002-292273/33.  
 XX  
 PT New nucleic acid oligomer, useful for detecting selected regions of gag  
 PT and pol genes of human immune deficiency virus, particularly for  
 XX assessing drug resistance.  
 XX  
 PS Claim 1; Page 38; 82pp; English.  
 CC  
 CC The present invention provides a number of nucleic acid oligomers which  
 CC can be used to amplify the gag and pol genes of human immunodeficiency  
 CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol  
 CC genes, especially regions associated with drug resistance, and also for  
 CC identifying genetic subtypes of the virus. The present sequence is an  
 CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS  
 CC field)  
 SQ Sequence 52 BP; 16 A; 14 C; 8 G; 14 T; 0 U; 0 Other;  
 Query Match 61.2%; Score 31.8; DB 6; Length 52;  
 Best Local Similarity 76.5%; Pred. No. 0.00085;  
 Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 AATTATAGCACTCATATAGGAGACGGGCGCCAACTGCTAGGATTT 51  
 Db 1 AATTATAGCACTCATATAGGAGACGGGCGCCAACTGCTAGGATTT 51  
 RESULT 12  
 ID AAA76206 standard; DNA; 49 BP.  
 XX  
 AC AAA76206;  
 XX  
 DT 25-JUN-2001 (first entry)  
 XX  
 DE Human prostate specific antigen PCR primer SEQ ID NO: 35.  
 XX  
 KW Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;  
 KW glandular kallikrein-2; hK2; prostate cancer; breast cancer; probe;  
 XX PCR primer; ss.  
 OS Homo sapiens.  
 PN WO200044940-A2.  
 PD 03-AUG-2000.  
 XX  
 PF 28-JAN-2000; 2000WO-US002270.  
 XX  
 PR 28-JAN-1999; 99US-0117640P.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Clark TJ;  
 XX  
 DR WPI; 2000-505986/45.  
 XX  
 PT Detecting prostate-specific antigen (PSA) prostate specific membrane  
 PT antigen (PSMA) or human kallikrein 2 (hK2) nucleic acids in samples using  
 PT probe molecules, useful for the diagnosis of prostate and breast cancers.  
 XX  
 PS Claim 1; Page 13; 77pp; English.  
 CC  
 CC The present invention is concerned with the detection of nucleic acid  
 CC markers for prostate and breast cancer, and PCR primers and probes which  
 CC are able to detect and quantify these markers. Prostate specific antigen  
 CC (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein  
 CC -2 (hK2) have all been linked to prostate and breast cancer, and the  
 CC primers and probes of the invention are able to detect the abnormal  
 CC presence of mRNA expressed by their coding sequences in tissues other

CC than the prostate. This enables the presence of cancer to be perceived  
 CC and aids in the detection of metastases  
 XX  
 SQ Sequence 49 BP; 17 A; 10 C; 10 G; 12 T; 0 U; 0 Other;  
 Query Match 60.4%; Score 31.4; DB 3; Length 49;  
 Best Local Similarity 85.4%; Pred. No. 0.0012;  
 Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 AATTATAGCACTCATATAGGAGACGGGCGCCAACTG 41  
 Db 2 AATTATAGCACTCATATAGGAGACGGGCGCCAACTG 42  
 RESULT 13  
 ID AAA63315 standard; DNA; 52 BP.  
 XX  
 AC AAA63315;  
 XX  
 DT 15-FEB-2001 (first entry)  
 XX  
 DE Mycobacterium avium paratuberculosis 23S gene PCR primer MPnae798R.  
 XX  
 KW Johne's disease; Crohn's disease; subspecies detection; 23S rRNA;  
 KW PCR primer; ss.  
 OS Mycobacterium avium subsp. paratuberculosis.  
 PN WO200034517-A1.  
 PD 15-JUN-2000.  
 XX  
 PF 03-DEC-1999; 99WO-NL000741.  
 XX  
 PR 04-DEC-1998; 98EP-00204117.  
 XX  
 PA (MICR-) MICROSCREEN BV.  
 PA (GEZO-) GEZONDHEIDSDIENST DIJREN.  
 PI Schut F, Ensing HZ, Koopmans HH, Tan PST, Wagter LHA;  
 PI Brinkhof JMA, Van Maanen C;  
 XX  
 DR WPI; 2000-423446/36.  
 XX  
 PT Detection of Mycobacterium avium paratuberculosis by identification of  
 PT specific 23S rRNA mutations at positions 754, 1363 or 3093 useful for  
 PT diagnosis of Johne's disease.  
 XX  
 PS Example 1; Fig 6; 81pp; English.  
 CC  
 CC The present sequence is a PCR primer used in the amplification of the  
 CC Mycobacterium avium subsp. paratuberculosis 23S rRNA gene. This gene  
 CC contains several mutations when compared to other Mycobacterium avium  
 CC subspecies, and some are unique enough to allow the development of a  
 CC probe which enables specific identification of the presence of a  
 CC paratuberculosis. The organism is responsible for Johne's disease in  
 CC ruminants, especially cows, and is possibly transmitted to humans where  
 CC it may lead to Crohn's disease. Efficient detection of the bacterium,  
 CC using a probe designed using this sequence, can be used to identify  
 CC infected animals so that they can be removed from the herd and destroyed  
 XX  
 SQ Sequence 52 BP; 15 A; 12 C; 13 G; 12 T; 0 U; 0 Other;  
 Query Match 60.4%; Score 31.4; DB 3; Length 52;  
 Best Local Similarity 85.4%; Pred. No. 0.0013;  
 Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 AATTATAGCACTCATATAGGAGACGGGCGCCAACTG 41  
 Db 2 AATTATAGCACTCATATAGGAGACGGGCGCCAACTG 42



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 01:14:18 ; Search time 2634.44 Seconds  
(without alignments)  
589.436 Million cell updates/sec

Title: US-10-001-407-15

Perfect score: 52  
Sequence: 1 aacttaactgactcactat.....gcccaactgctaggatttc 52

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 569298

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST: \*  
1: em\_estba: \*  
2: em\_estbm: \*  
3: em\_estin: \*  
4: em\_estmu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_hic: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_hic: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estum: \*  
16: em\_estom: \*  
17: em\_gss\_hum: \*  
18: em\_gss\_inv: \*  
19: em\_gss\_pln: \*  
20: em\_gss\_vrt: \*  
21: em\_gss\_fun: \*  
22: em\_gss\_mam: \*  
23: em\_gss\_mus: \*  
24: em\_gss\_pro: \*  
25: em\_gss\_rod: \*  
26: em\_gss\_phg: \*  
27: em\_gss\_vrl: \*  
28: gb\_gss1: \*  
29: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	50.0	79	9	AJ282930 4A3A-PIE1
2	25.6	49.2	100	9	AJ353756 zeh0940.8
3	25.6	49.2	100	29	CG728851 1119104C1
4	25.4	48.8	87	14	CA406952 1003101 H

5	25.4	48.8	90	29	CG732206	CG732206 1119146G0
6	25.2	47.5	98	29	CG729102	CG729102 1119107G0
7	24.6	47.3	96	9	A1616894	A1616894 zeh0783.
8	23.8	45.8	75	9	A1087772	A1087772 SKOVAMCAQ
9	23.8	45.8	79	14	CA336070	CA336070 NISC_1u07
10	23.6	45.4	86	29	CG733887	CG733887 1119160E1
11	23.6	45.4	90	29	CG732908	CG732908 1119152D0
12	23.6	45.4	95	9	A1353162	A1353162 zeh0113.8
13	23.6	45.4	95	9	A1353583	A1353583 zeh0701.8
14	23.6	45.4	96	9	A1617314	A1617314 zeh11391.
15	23.6	45.4	96	10	AW455598	AW455598 zeh11725
16	23.6	45.4	100	29	CG729011	CG729011 1119106D0
17	23.6	45.4	100	29	CG729055	CG729055 1119107A0
18	23.4	45.0	76	14	CF651968	CF651968 26-102013
19	23	44.2	30	28	AO797214	AO797214 RPCI -22-4
20	22.8	43.8	55	14	CB261880	CB261880 83-E8880-
21	22.8	43.8	96	14	R29179	R29179 F1-287D 22
22	22.4	43.1	86	29	CG807118	CG807118 1118077H0
23	22.4	43.1	88	29	CG728803	CG728803 1119103C1
24	22.4	43.1	89	14	N88337	N88337 K313P Huma
25	22.4	43.1	97	9	AA051807	AA051807 SWAMCA143
26	22.4	43.1	100	29	CG728814	CG728814 1119103E1
27	22.4	43.1	100	29	CG729247	CG729247 1119110B0
28	22.4	43.1	100	29	CG731464	CG731464 1119140G1
29	22.4	43.1	100	29	CG732356	CG732356 1119147G1
30	22.2	42.7	51	14	CD005157	CD005157 VVB049D11
31	22.2	42.7	54	29	CG807965	CG807965 1118088C1
32	22.2	42.7	55	14	CB263019	CB263019 38-E8881-
33	22.2	42.7	61	13	BU634607	BU634607 009H07 In
34	22.2	42.7	66	14	CD288815	CD288815 7 N19. abd
35	22.2	42.7	72	29	CG731440	CG731440 1119140E1
36	22.2	42.7	73	9	AA680645	AA680645 LmfFram09
37	22.2	42.7	77	13	BU634641	BU634641 012F12 In
38	22.2	42.7	78	29	CG732916	CG732916 1119152F0
39	22.2	42.7	78	29	CG799906	CG799906 1118005B0
40	22.2	42.7	80	9	AJ494595	AJ494595 AJ494595
41	22.2	42.7	80	14	CB262186	CB262186 71-E9724-
42	22.2	42.7	86	29	CG799851	CG799851 1118005B0
43	22.2	42.7	86	29	CG807595	CG807595 1118058B1
44	22.2	42.7	87	14	CF200277	CF200277 G1T1279 R
45	22.2	42.7	87	29	CG729167	CG729167 1119108G0

## ALIGNMENTS

RESULT 1  
AJ282930 79 bp mRNA linear EST 30-JUN-2000  
LOCUS 4A3A-PIE1-R Anopheles gambiae immune competent 4A3A Anopheles  
DEFINITION gambiae CDNA clone 4A3A-PIE1, mRNA sequence.  
ACCESSION AJ282930 GI:6930809  
VERSION AJ282930.1  
KEYWORDS EST.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;  
Anopheles.  
REFERENCE 1 (bases 1 to 79)  
Dimopoulos G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C.,  
Donohue, M., Schultz, J., Benez, V., Bork, P., Ambrose, W., Soares, M.B.  
and Kafatos, F.C.  
Anopheles gambiae pilot gene discovery project: identification of  
mosquito innate immunity genes from expressed sequence tags  
generated from immune-competent cell lines  
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)

JOURNAL MEDLINE  
PUBMED  
10841561  
Contact: Dimopoulos G  
Fotis C. Kafatos laboratory  
European Molecular Biology Laboratory  
Meyerothofstrasse 1, 69117 Heidelberg, Germany.

## FEATURES

Location/Qualifiers

1..79  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="4A r/r"  
/db\_xref="taxon:7165"  
/clone="4A3A-PIE1"  
/cell\_line="immune competent 4A3A"  
/lab\_host="E. coli DH10B"  
/note="Anopheles gambiae immune competent 4A3A"  
polylinker Site\_1: EcoRI; Site\_2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA library that was constructed from the 4A3A cell line oligo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996) : Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."

## ORIGIN

Query Match 50.0%; Score 26; DB 9; Length 79;  
Best Local Similarity 85.3%; Pred. No. 13;  
Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGACGGCGCC 34  
28 AATTATACGACTCACTATAGGAGATTGGCCC 61

RESULT 2 100 bp mRNA linear EST 04-JAN-1999  
A1353756 zeh0940.seq.F Zebrafish Embryonic Heart cDNA library Danio rerio  
LOCUS CDNA 5', mRNA sequence.  
ACCESSION A1353756  
KEYWORDS A1353756.1 GI:4093909  
EST.

SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Osteichthyes;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 100)  
Tom,C., Mabiy,J.D., Dempsey,A.A., Hwang,D.M., Fishman,M.C. and  
Liew,C.C.

REFERENCE Identification and Characterization of Expressed Sequence Tags from  
an Embryonic Zebrafish Heart cDNA Library  
JOURNAL Unpublished (1999)  
COMMENT Contact: Liew CC  
Brigham and Women's Hospital  
Harvard Medical School  
75 Francis St. Boston, MA 02115, USA  
Tel: 6177328915  
Fax: 6179750995  
Email: cliw@rics.bwh.harvard.edu  
PCR Primers  
FORWARD: 5' GCCAGCTCGAATTAACCTCACTAAAGG 3'  
BACKWARD: 5' CCGATGATGTAATGACCTCACTAAGGCG 3'  
Seq primer: 5' GAATTAACCTCACTAAAGG 3'.  
Location/Qualifiers  
1..100

FEATURES  
SOURCE /organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/dev\_stage="embryonic day 3 post-fertilization"  
/lab\_host="E.coli XL1-Blue mF"  
/clone\_lib="Zebrafish Embryonic Heart cDNA library"  
/note="Organ: heart; Vector: lambda ZAP Express; Site\_1:  
EcoRI; Site\_2: XhoI; mRNA was purified from embryonic  
zebrafish hearts (3 day post-fertilization). cDNA was  
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI  
adaptors were ligated, followed by digestion with XhoI,  
for directional cloning into pre-digested lambda ZAP

## ORIGIN

Express vector. "

Query Match 49.2%; Score 25.6; DB 9; Length 100;  
Best Local Similarity 70.8%; Pred. No. 20;  
Matches 34; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGACGGCGCCCACTGTAAGGA 48  
98 AATTATACGACTCACTATAGGAGCAATTGGGATCACTTACTGGA 51

RESULT 3 100 bp DNA linear GSS 20-OCT-2003  
CG728851 119104C10.1EL.X1 1119 - RescueMu Grid AA Zee mays genomic, genomic  
survey sequence.  
LOCUS CG728851  
DEFINITION CG728851.1 GI:37769986  
GSS.

ACCESSION CG728851  
VERSION CG728851  
KEYWORDS Zee mays  
SOURCE Zee mays  
ORGANISM Zee mays  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zae.  
1 (bases 1 to 100)  
Walbot,V.

REFERENCE Malze genomic sequences found using engineered RescueMu transposon  
AUTHORS Unpublished (2001)  
TITLE Contact: Walbot V  
JOURNAL Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 119104 row: 12  
Class: transposon-tagged.  
Location/Qualifiers  
1..100

FEATURES  
SOURCE /organism="Zee mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73/K55"  
/db\_xref="taxon:4577"  
/issue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1119 - RescueMu Grid AA"  
/note="Organ: leaf; Vector: RescueMu (engineered from  
pBluescript backbone); Site\_1: BamHI; Site\_2: BglII;  
RescueMu is a 4.9 Kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic  
Mu elements insert preferentially into transcripion  
units. For more information on RescueMu, go to the web  
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA  
was extracted from leaf strips, double digested using  
BamHI and BglII, and ligated to form circular plasmids.  
DH10B cells were transformed and then screened on LB  
plates with ampicillin."

## ORIGIN

Query Match 49.2%; Score 25.6; DB 29; Length 100;  
Best Local Similarity 70.8%; Pred. No. 20;  
Matches 34; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGACGGCGCCCACTGTAAGGA 48  
29 AATTATACGACTCACTATAGGAGCAATTGGGAGAGACGGCGGTGA 76

RESULT 4  
CA406952/c  
LOCUS CA406952 87 bp mRNA linear EST 07-NOV-2002  
DEFINITION 1003101 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens  
CDNA 5', mRNA sequence.  
ACCESSION CA406952  
VERSION CA406952.1 GI:24771823  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 87)  
AUTHORS Yang, R.-Z., Shuldiner, A. and Gong, D.-W.  
TITLE EST analysis of human adipose gene expression  
JOURNAL Unpublished (2002)  
COMMENT Contact: Gong Da-Wei  
Division of Endocrinology, Diabetes and Nutrition  
University of Maryland  
660 Redwood St. HH497, Baltimore, MD 21201, USA  
Tel: 410 706 1672  
Fax: 410 706 1622  
Email: dgong@medicine.umaryland.edu  
PCR Primers  
FORWARD: CTCGGGAGCGCGCATTTGTTGGT  
REVERSE: ATATGAGCTCACTATATGCGCAATTGG  
Seq primer: GTTGGTACCGGGAATTC.  
Location/Qualifiers  
1..87  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/sex="Male and Female"  
/tissue\_type="Adipose"  
/clone\_id="Human Fat Cell 5'-Stretch Plus cDNA Library"  
/note="Vector: lambdaTriplex"

ORIGIN

Query Match 48.8%; Score 25.4; DB 14; Length 87;  
Best Local Similarity 82.9%; Pred. No. 22;  
Matches 29; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TTTATACGACTCACTATAGGAGAGCGGCGCA 37  
|||||  
Db 86 TTTATACGACTCACTATAGGAGCGGCGCA 52  
|||||

RESULT 5  
CG732206 90 bp DNA linear GSS 20-OCT-2003  
LOCUS 1119146G02.1EL.X1 1119 - Rescemu Grid AA Zea mays genomic, genomic  
DEFINITION Survey sequence.  
ACCESSION CG732206  
VERSION CG732206.1 GI:37774698  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 90)  
AUTHORS Walbot, V.  
TITLE Maize genomic sequences found using engineered Rescemu transposon  
JOURNAL Unpublished (2001)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Very probable ligation site of ends cut by single endonuclease.  
Reverse complemented post-ligation sequence from source sequence.

Plate: 1119146 column: 36  
Class: transposon-tagged.  
Location/Qualifiers  
1..90  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultiivar="mixed background W23/A186/B73/K55"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_id="1119 - Rescemu Grid AA"  
/note="Organ: leaf; Vector: Rescemu (engineered from  
pBluescript backbone); Site 1: BamHI; Site 2: BglII;  
Rescemu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on Rescemu, go to the web  
site 'www.zmdb.laestate.edu' and follow the links for  
'Rescemu.' Grid AA was grown at UC San Diego in 2002. DNA  
was extracted from leaf strips, double digested using  
BamHI and BglII, and ligated to form circular plasmids.  
DH10B cells were transformed and then screened on LB  
plates with ampicillin."

ORIGIN

Query Match 48.8%; Score 25.4; DB 29; Length 90;  
Best Local Similarity 96.3%; Pred. No. 23;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCACTATAGGAGAGA 27  
|||||  
Db 19 AATTATACGACTCACTATAGGAGCA 45  
|||||

RESULT 6  
CG729102 98 bp DNA linear GSS 20-OCT-2003  
LOCUS 1119107G02.1EL.X1 1119 - Rescemu Grid AA Zea mays genomic, genomic  
DEFINITION Survey sequence.  
ACCESSION CG729102  
VERSION CG729102.1 GI:37770478  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 98)  
AUTHORS Walbot, V.  
TITLE Maize genomic sequences found using engineered Rescemu transposon  
JOURNAL Unpublished (2001)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Very probable ligation site of ends cut by single endonuclease.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1119107 row: 3  
Class: transposon-tagged.  
Location/Qualifiers  
1..98  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultiivar="mixed background W23/A186/B73/K55"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_id="1119 - Rescemu Grid AA"

/note="Organ: leaf; Vector: RescuenMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescuenMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescuenMu, go to the web site 'www.zmbl.jastate.edu' and follow the links for 'RescuenMu.' Grid Aa was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## ORIGIN

Query Match 48.5%; Score 25.2; DB 29; Length 98;  
Best Local Similarity 78.9%; Pred. No. 28;  
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AATTATAGACTCTATTAGGAGCGGCGCCCAAC 38  
DB 27 AATTATAGACTCTATTAGGAGCGGCGCCCAAC 64

RESULT 7 96 bp mRNA linear EST 21-APR-1999  
A1616894  
LOCUS zehno783.seq.F Zebrafish Embryonic Heart cDNA Library Danilo rerio  
DEFINITION cDNA 5', mRNA sequence.  
ACCESSION A1616894  
VERSION A1616894.1 GI:4626061  
KEYWORDS EST.  
SOURCE Danilo rerio (zebrafish)  
ORGANISM Danio rerio

REFERENCE 1 (bases 1 to 96)  
AUTHORS Ton, C., Mabry, J.D., Dempsey, A.A., Hwang, D.M., Fishman, M.C. and Liaw, C.C.  
TITLE Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library  
JOURNAL Unpublished (1999)  
COMMENT Contact: Liaw, CC  
Brigham and Women's Hospital  
Harvard Medical School  
75 Francis St., Boston, MA 02115, USA  
Tel: 6177328915  
Fax: 6179750995  
Email: ctlew@rics.bwh.harvard.edu

PCR Primers  
FORWARD: 5' GCCAGCTCGAATTAACTCTACTTAAGGG 3'  
BACKWARD: 5' CCAAGTGAATGTATAGACTCTACTTAAGGG 3'  
Seq primer: 5' GAATTACCTCTACTTAAGGG 3'.  
FEATURES  
source  
1..96  
location/Qualifiers  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/dev\_stage="embryonic day 3 post-fertilization"  
/lab\_host="B.coli XL1-Blue mrf."  
/clone\_idb="zebrafish Embryonic Heart cDNA Library"  
/note="Organ: heart; Vector: Lambda ZAP Express; Site\_1: EcoRI; Site\_2: XhoI; mRNA was purified from embryonic zebrafish hearts (3 day post-fertilization). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into pre-digested Lambda ZAP Express vector."

## ORIGIN

Query Match 47.3%; Score 24.6; DB 9; Length 96;  
Best Local Similarity 70.2%; Pred. No. 47;  
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 2 AATTATAGACTCTATTAGGAGCGGCGCCCAACTGCTAGGA 48  
DB 96 AATTATAGACTCTATTAGGAGCGGCGCAATTGGTACTACTCTGTA 50

RESULT 8 75 bp mRNA linear EST 18-AUG-1998  
A1087772  
LOCUS SMOVAMCAQ02F02SK Onchocerca volvulus adult male cDNA  
DEFINITION (SM99MMLV-OVM) Onchocerca volvulus cDNA clone SMOVAMCAQ02F02 5', mRNA sequence.  
ACCESSION A1087772  
VERSION A1087772.1 GI:3426748  
KEYWORDS EST.  
SOURCE Onchocerca volvulus  
ORGANISM Onchocerca volvulus

REFERENCE 1 (bases 1 to 75)  
AUTHORS Lizotte-Waniewski, M. and Williams, S.A.  
TITLE Genes expressed in adult male stage of Onchocerca volvulus  
JOURNAL Unpublished (1998)  
COMMENT Contact: Steven A. Williams  
Molecular Parasitology  
Smith College Department of Biological Sciences  
Department of Biological Sciences, Clark Science Center, Smith  
College, Northampton, MA, 01063, USA  
Tel: 4135853826  
Fax: 4135853786  
Email: genome@smith.edu

FEATURES  
source  
Seq primer: pInuescript SK.  
Location/Qualifiers  
1..75  
/organism="Onchocerca volvulus"  
/mol\_type="mRNA"  
/db\_xref="taxon:6282"  
/clone="SMOVMCAQ02F02"  
/sex="male"  
/dev\_stage="adult"  
/lab\_host="XL1-Blue MRF"  
/clone\_idb="Onchocerca volvulus adult male cDNA (SM99MMLV-OVM)"

/note="Vector: Lambda Uni-ZAP XR; Site\_1: Eco RI; Site\_2: Xho I; Filarial nematode parasite of humans. Six adult male worms of Onchocerca volvulus were isolated from consenting patients and quick frozen. Adult male mRNA was converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 2 x 10<sup>5</sup> independent recombinants and the average insert size is ~1100bp. The library was constructed by Michelle Lizotte-Waniewski with worms provided by Dr. Sara Lustigman. The library is available from Dr. Steven A. Williams, email: genome@smith.edu."

## ORIGIN

Query Match 45.8%; Score 23.8; DB 9; Length 75;  
Best Local Similarity 92.6%; Pred. No. 87;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATTATAGACTCTATTAGGAGGA 27  
DB 67 AATTATAGACTCTATTAGGAGGA 41

RESULT 9 79 bp mRNA linear EST 04-NOV-2002  
CA336070  
LOCUS NISC\_Lu07h08.v1 COGENE 4AR (4EAR) Homo sapiens cDNA clone  
DEFINITION IMAGE:5607422 5', mRNA sequence.  
ACCESSION CA336070  
VERSION CA336070.1 GI:24554168  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS 1 (bases 1 to 79)  
TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
COMMENT Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
CDNA Library Preparation:  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[info@image.llnl.gov](mailto:info@image.llnl.gov)  
Plate: LHAM12408 row: P column: 15  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
1..79  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_image="5607422"  
/tissue\_type="anterior rhombomeres 1-4 (4 pooled)"  
/dev\_stage="embryo, 4 weeks postconception"  
/lab\_host="DH10B"  
/clone\_lib="COGENE 4AR (4EAR)"  
/note="Vector: pAMP1; cDNA primed using oligo-dT primer,  
directionally cloned into UDG sites of pAMP1. Size  
selected for insert sizes ranging from 0.3-1.6 kb.  
Normalized to Col10. Primary library, non-emplified.  
Library constructed by M. Lovett. For more information on  
this library, please contact R. Tidwell (Washington  
University) or visit the COGENE website at  
<http://hg.wustl.edu/COGENE/>."

ORIGIN  
Query Match 45.8%; Score 23.6; DB 14; Length 79;  
Best Local Similarity 92.6%; Pred. No. 89;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTTAATACGACTCACTATAGGAGACG 29  
|||||  
40 TTTAATACGACTCACTATAGGAGTCG 14  
|||||

RESULT 10  
CG733887 86 bp DNA linear GSS 20-OCT-2003  
LOCUS 1119160E0.1EL.X1 1119 - Rescemu Grid AA Zea mays genomic, genomic  
DEFINITION survey sequence.  
ACCESSION CG733887  
VERSION CG733887.1 GI:37776379  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
TITLE clade; Panicoidae; Andropogoneae; Zea.  
JOURNAL 1 (bases 1 to 86)  
COMMENT Walbot, V.  
Maize genomic sequences found using engineered Rescemu transposon  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: [walbot@stanford.edu](mailto:walbot@stanford.edu)

Very probable ligation site of ends cut by single endonuclease.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1119160 row: 14  
Class: transposon-tagged.  
Location/Qualifiers  
1..86  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultiivar="mixed background W23/A188/B73/K55"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1119 - Rescemu Grid AA"  
/note="Organ: leaf; Vector: Rescemu (engineered from  
pBluescript backbone); Site 1: BamHI, Site 2: BglII;  
Rescemu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on Rescemu, go to the web  
site 'www.zmdb.ucsd.edu' and follow the links for  
'Rescemu.' Grid AA was grown at UC San Diego in 2002. DNA  
was extracted from leaf strips, double digested using  
BamHI and BglII, and ligated to form circular plasmids.  
DH10B cells were transformed and then screened on LB  
plates with ampicillin."

ORIGIN  
Query Match 45.4%; Score 23.6; DB 29; Length 86;  
Best Local Similarity 76.3%; Pred. No. 11e+02;  
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGCGGCCCAAC 38  
|||||  
15 AATTATACGACTCACTATAGGCGATTTCACAGACG 52  
|||||

Db 15 AATTATACGACTCACTATAGGCGATTTCACAGACG 52  
|||||

RESULT 11  
CG732908 90 bp DNA linear GSS 20-OCT-2003  
LOCUS 1119152D09.1EL.X1 1119 - Rescemu Grid AA Zea mays genomic, genomic  
DEFINITION survey sequence.  
ACCESSION CG732908  
VERSION CG732908.1 GI:37775400  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
TITLE clade; Panicoidae; Andropogoneae; Zea.  
JOURNAL 1 (bases 1 to 90)  
COMMENT Walbot, V.  
Maize genomic sequences found using engineered Rescemu transposon  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: [walbot@stanford.edu](mailto:walbot@stanford.edu)  
Very probable ligation site of ends cut by single endonuclease.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1119152 row: 14  
Class: transposon-tagged.  
Location/Qualifiers  
1..90  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultiivar="mixed background W23/A188/B73/K55"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"

/lab host="DH10B"  
 /clone\_lib="1119 - RescueMu Grid AA"  
 /note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmmb.iastate.edu' and follow the links for 'RescueMu'. Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## ORIGIN

Query Match 45.4%; Score 23.6; DB 29; Length 90;  
 Best Local Similarity 76.3%; Pred. No. 1.1e+02;  
 Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 AATTATACGACTACTATAGGAGACGGGCGCCCAAC 38  
 19 ATTGTATACGACTACTATAGGCGCTCTGCGCGAC 56

RESULT 12  
 A1353162 95 bp mRNA linear EST 04-JAN-1999  
 LOCUS zeh0113.seq.F Zebrafish Embryonic Heart cDNA Library Danio rerio  
 DEFINITION CDNA 5', mRNA sequence.  
 ACCESSION A1353162  
 VERSION A1353162.1 GI:4093315  
 KEYWORDS EST  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Danio rerio

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 95)  
 Ton, C., Mably, J.D., Dempsey, A.A., Hwang, D.M., Fishman, M.C. and Liew, C.C.

TITLE Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Liew CC  
 Brigham and Women's Hospital  
 Harvard Medical School  
 75 Francis St. Boston, MA 02115, USA  
 Tel: 6177328915  
 Fax: 6179750995  
 Email: clliew@rics.bwh.harvard.edu

PCR Primers  
 FORWARD: 5' GCCAGCTCGAATTAACCTCTCAAGG 3'  
 BACKWARD: 5' CCAGTGAATTGATATACGACTCACTAAGGCG 3'  
 Seq primer: 5' GAAATTAACCTCACTAAGG 3'.  
 Location/Qualifiers

## FEATURES

SOURCE

1..95  
 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /dev\_stage="embryonic day 3 post-fertilization"  
 /lab\_host="E.coli XL1-Blue mrf"  
 /clone\_lib="Zebrafish Embryonic Heart cDNA Library"  
 /note="Organ: heart; Vector: lambda ZAP Express; Site 1: EcoRI; Site 2: XhoI; mRNA was purified from embryonic zebrafish hearts (3 day post-fertilization). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into pre-digested lambda ZAP Express vector."

## ORIGIN

Query Match

45.4%; Score 23.6; DB 9; Length 95;

Best Local Similarity 69.6%; Pred. No. 1.1e+02;  
 Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
 Qy 3 TTATATACGACTACTATAGGAGACGGGCGCCCACTGCTAGGA 48  
 95 TGTATATACGACTACTATAGGCGAATGGGTACCTTACTCGTA 50

RESULT 13  
 A1353583 95 bp mRNA linear EST 04-JAN-1999  
 LOCUS zeh0701.seq.F Zebrafish Embryonic Heart cDNA Library Danio rerio  
 DEFINITION CDNA 5', mRNA sequence.  
 ACCESSION A1353583  
 VERSION A1353583.1 GI:4093736  
 KEYWORDS EST  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Danio rerio

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 95)  
 Ton, C., Mably, J.D., Dempsey, A.A., Hwang, D.M., Fishman, M.C. and Liew, C.C.

TITLE Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Liew CC  
 Brigham and Women's Hospital  
 Harvard Medical School  
 75 Francis St. Boston, MA 02115, USA  
 Tel: 6177328915  
 Fax: 6179750995  
 Email: clliew@rics.bwh.harvard.edu

PCR Primers  
 FORWARD: 5' GCCAGCTCGAATTAACCTCTCAAGG 3'  
 BACKWARD: 5' CCAGTGAATTGATATACGACTCACTAAGGCG 3'  
 Seq primer: 5' GAAATTAACCTCACTAAGG 3'.  
 Location/Qualifiers

## FEATURES

SOURCE

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 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /dev\_stage="embryonic day 3 post-fertilization"  
 /lab\_host="E.coli XL1-Blue mrf"  
 /clone\_lib="Zebrafish Embryonic Heart cDNA Library"  
 /note="Organ: heart; Vector: lambda ZAP Express; Site 1: EcoRI; Site 2: XhoI; mRNA was purified from embryonic zebrafish hearts (3 day post-fertilization). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into pre-digested lambda ZAP Express vector."

## ORIGIN

Query Match 45.4%; Score 23.6; DB 9; Length 95;  
 Best Local Similarity 69.6%; Pred. No. 1.1e+02;  
 Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 3 TTATATACGACTACTATAGGAGACGGGCGCCCACTGCTAGGA 48  
 95 TGTATATACGACTACTATAGGCGAATGGGTACCTTACTCGTA 50

RESULT 14  
 A1617314 96 bp mRNA linear EST 21-APR-1999  
 LOCUS zeh1391.seq.F Zebrafish Embryonic Heart cDNA Library Danio rerio  
 DEFINITION CDNA 5', mRNA sequence.  
 ACCESSION A1617314  
 VERSION A1617314.1 GI:4626481  
 KEYWORDS EST  
 SOURCE Danio rerio (zebrafish)



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 01:28:53 ; Search time 81.7143 Seconds  
(without alignments)  
353.151 Million cell updates/sec

Title: US-10-001-407-15

Perfect score: 52  
Sequence: 1 aatttaatacgaactcactat.....gccaaactgctaggatttc 52

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 939290

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
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2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PTCUTS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfillseq1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36.4	70.0	50	4	US-09-611-627-8 Sequence 8, Appli
2	36.4	70.0	51	4	US-09-611-627-26 Sequence 26, Appli
3	36	69.2	54	4	US-09-168-947-2 Sequence 2, Appli
4	31.8	61.2	52	4	US-09-944-036-7 Sequence 7, Appli
5	31.4	60.4	49	4	US-09-493-491-35 Sequence 35, Appli
6	31.4	60.4	49	4	US-09-493-491A-38 Sequence 38, Appli
7	30.4	58.5	52	4	US-09-168-947-15 Sequence 15, Appli
8	30.2	58.1	53	4	US-09-944-036-5 Sequence 5, Appli
9	30.2	58.1	53	4	US-09-944-036-37 Sequence 37, Appli
10	29.8	57.3	48	4	US-09-040-220D-7 Sequence 7, Appli
11	29.8	57.3	48	4	US-09-265-686-7 Sequence 7, Appli
12	29.8	57.3	48	4	US-09-723-749-7 Sequence 7, Appli
13	29.6	56.9	47	1	US-08-162-836-10 Sequence 10, Appli
14	29.6	56.9	47	1	US-08-345-861-6 Sequence 6, Appli
15	29.6	56.9	47	2	US-08-479-105A-6 Sequence 6, Appli
16	29.6	56.9	47	3	US-09-502-966-3 Sequence 3, Appli
17	29.2	56.2	45	4	US-09-166-947-39 Sequence 39, Appli
18	28.8	55.4	49	4	US-09-611-627-24 Sequence 24, Appli
19	28.8	55.4	49	4	US-09-611-627-28 Sequence 28, Appli
20	28.8	55.4	50	2	US-08-448-267A-1 Sequence 1, Appli
21	28.8	55.4	50	4	US-09-944-036-8 Sequence 8, Appli
22	28.8	55.4	53	1	US-08-384-541-13 Sequence 13, Appli
23	28.8	55.4	53	1	US-08-384-541-14 Sequence 14, Appli
24	28.8	55.4	53	1	US-08-384-541-15 Sequence 15, Appli
25	28.8	55.4	53	1	US-08-384-541-16 Sequence 16, Appli
26	28.2	54.2	46	2	US-08-448-267A-6 Sequence 6, Appli
27	28.2	54.2	51	4	US-09-168-947-25 Sequence 25, Appli

28	28	53.8	32	1	US-08-482-428-14 Sequence 14, Appli
29	28	53.8	32	1	US-08-486-705-14 Sequence 14, Appli
30	28	53.8	32	1	US-09-944-036-3 Sequence 3, Appli
31	28	53.8	35	2	US-08-360-051A-23 Sequence 23, Appli
32	28	53.8	35	4	US-09-202-972-16 Sequence 16, Appli
33	28	53.8	45	1	US-08-692-610-3 Sequence 3, Appli
34	28	53.8	45	1	US-08-692-610-3 Sequence 3, Appli
35	28	53.8	45	1	US-08-421-471-4 Sequence 4, Appli
36	28	53.8	45	1	US-08-683-124-3 Sequence 3, Appli
37	28	53.8	48	1	US-08-162-836-6 Sequence 6, Appli
38	28	53.8	48	4	US-09-710-200-7 Sequence 7, Appli
39	28	53.8	48	4	US-09-975-408-7 Sequence 7, Appli
40	28	53.8	49	1	US-08-384-541-5 Sequence 5, Appli
41	28	53.8	49	1	US-08-384-541-6 Sequence 6, Appli
42	28	53.8	49	1	US-08-384-541-7 Sequence 7, Appli
43	28	53.8	49	1	US-08-384-541-8 Sequence 8, Appli
44	28	53.8	49	1	US-08-692-610-2 Sequence 2, Appli
45	28	53.8	49	1	US-08-683-122-2 Sequence 2, Appli

## ALIGNMENTS

```
RESULT 1
US-09-611-627-8
; Sequence 8, Application US/09611627
; Patent No. 6623920
; GENERAL INFORMATION:
; APPLICANT: BEE, Gary G.
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: KOIK, Dan
; APPLICANT: GINCHETTI, Cristina
; APPLICANT: MCDONOUGH, Sherrol H.
; TITLE OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
; FILE REFERENCE: GP103-02.UT
; CURRENT APPLICATION NUMBER: US/09/611.627
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/143.072
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amplification oligomer with 5' promoter sequence,
; OTHER INFORMATION: for HIV-1 LTR region
US-09-611-627-8
Query Match 70.0%; Score 36.4; DB 4; Length 50;
Best Local Similarity 94.2%; Pred. No. 1.1e-06;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
Cy 1 AATTATATGACCTACTTATGAGAGCGGCGCCACCTCTGCGATTTC 52
Db 1 AATTATATGACCTACTTATGAGAGCGGCGCCACCTCTGCGATTTC 50
RESULT 2
US-09-611-627-26
; Sequence 26, Application US/09611627
; Patent No. 6623920
; GENERAL INFORMATION:
; APPLICANT: BEE, Gary G.
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: KOIK, Dan
; APPLICANT: GINCHETTI, Cristina
; APPLICANT: MCDONOUGH, Sherrol H.
; TITLE OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
; FILE REFERENCE: GP103-02.UT
; CURRENT APPLICATION NUMBER: US/09/611.627
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;; CURRENT FILING DATE: 2000-07-07  
;; PRIOR APPLICATION NUMBER: 60/143,072  
;; PRIOR FILING DATE: 1998-07-09  
;; NUMBER OF SEQ ID NOS: 57  
;; SOFTWARE: Patentin Ver. 2.0  
;; SEQ ID NO 26  
;; LENGTH: 51  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
;; OTHER INFORMATION: amplification oligomer with 5' promoter sequence,  
us-09-611-627-26

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Best Local Similarity 70.0%; Score 36.4; DB 4; Length 51;  
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

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Db 1 AATTAAATACGACTCCTATAGGAGACGGCGCCCA--CTGCTAGGATTT 50

RESULT 3  
; Sequence 2, Application US/09168947  
; Patent No. 6589734  
; GENERAL INFORMATION:  
; APPLICANT: KACIAN, DANIEL L.  
; APPLICANT: FULTZ, TIMOTHY J.  
; APPLICANT: MCDONOUGH, SHERROL H.  
; TITLE OF INVENTION: DETECTION OF HIV  
; FILE REFERENCE: 218/130  
; CURRENT APPLICATION NUMBER: US/09/168,947  
; CURRENT FILING DATE: 1998-10-08  
; EARLIER APPLICATION NUMBER: 08/469,067  
; EARLIER FILING DATE: 1995-06-06  
; EARLIER APPLICATION NUMBER: 07/550,837  
; EARLIER FILING DATE: 1990-07-10  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 54  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized nucleic acid molecule  
us-09-168-947-2

Query Match  
Best Local Similarity 69.2%; Score 36; DB 4; Length 54;  
Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
Qy 1 AATTAAATACGACTCCTATAGGAGACGGCGCCCAACTGCTAGGATTT 52  
Db 1 AATTAAATACGACTCCTATAGGAGACGGAGACTTCCGCTGGGACTTT 52

RESULT 4  
; Sequence 7, Application US/09944036  
; Patent No. 6582920  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036

;; CURRENT FILING DATE: 2001-08-31  
;; PRIOR APPLICATION NUMBER: US 60/229,790  
;; PRIOR FILING DATE: 2000-09-01  
;; NUMBER OF SEQ ID NOS: 70  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO 7  
;; LENGTH: 52  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence:  
;; OTHER INFORMATION: Oligonucleotide primer for Protease target  
; NAME/KEY: Promoter  
; LOCATION: (1) .. (32)  
us-09-944-036-7

Query Match  
Best Local Similarity 61.2%; Score 31.8; DB 4; Length 52;  
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AATTAAATACGACTCCTATAGGAGACGGCGCCCAACTGCTAGGATTT 51  
Db 1 AATTAAATACGACTCCTATAGGAGACCCAGCCATTCCTCGCTTT 51

RESULT 5  
; Sequence 35, Application US/09493491  
; Patent No. 6391556  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491  
; CURRENT FILING DATE: 2000-01-28  
; EARLIER APPLICATION NUMBER: 60/117,640 US  
; EARLIER FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 49  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
us-09-493-491-35

Query Match  
Best Local Similarity 60.4%; Score 31.4; DB 4; Length 49;  
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 AATTAAATACGACTCCTATAGGAGACGGCGCCCAACTG 41  
Db 2 AAATTAAATACGACTCCTATAGGAGACTGTGCTGACTG 42

RESULT 6  
; Sequence 38, Application US/09493491A  
; Patent No. 6551778  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491A  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US

PRIOR FILING DATE: 1999-01-28  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 38  
LENGTH: 49  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
FEATURE:  
NAME/KEY: promoter  
LOCATION: (1)..(28)  
US-09-493-491A-38

Query Match 60.4%; Score 31.4; DB 4; Length 49;  
Best Local Similarity 85.4%; Pred. No. 0.0016;  
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATTATAGCACTACTATAGGAGCGGCGGCAACTG 41  
Db 2 AAATTATAGCACTACTATAGGAGCGGCTGACTG 42

RESULT 7  
US-09-168-947-15  
Sequence 15, Application US/09168947  
Patent No. 6589734  
GENERAL INFORMATION:  
APPLICANT: KACIAN, DANIEL L.  
APPLICANT: FULTZ, TIMOTHY J.  
APPLICANT: MCDONOUGH, SHERROL H.  
TITLE OF INVENTION: DETECTION OF HIV  
FILE REFERENCE: 218/130  
CURRENT APPLICATION NUMBER: US/09/168,947  
CURRENT FILING DATE: 1998-10-08  
EARLIER APPLICATION NUMBER: 08/469,067  
EARLIER FILING DATE: 1995-06-06  
EARLIER APPLICATION NUMBER: 07/550,837  
EARLIER FILING DATE: 1990-07-10  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 52  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized nucleic acid molecule  
US-09-168-947-15

Query Match 58.5%; Score 30.4; DB 4; Length 52;  
Best Local Similarity 85.0%; Pred. No. 0.00043;  
Matches 34; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATTATAGCACTACTATAGGAGCGGCGGCAACT 40  
Db 1 AATTATAGCACTACTATAGGAGCGGCTGCTCTT 40

RESULT 8  
US-09-944-036-5  
Sequence 5, Application US/09944036  
Patent No. 6582920  
GENERAL INFORMATION:  
APPLICANT: YANG, Yeasing Y.  
APPLICANT: BRENTANO, Steven T.  
APPLICANT: BABOLA, Odile  
APPLICANT: TRAN, Nathalie  
APPLICANT: VERNET, Guy  
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
FILE REFERENCE: GP114-02 UT  
CURRENT APPLICATION NUMBER: US/09/944,036

CURRENT FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/229,790  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: Oligonucleotide primer for Gag target sequence  
NAME/KEY: promoter  
LOCATION: (1)..(29)  
US-09-944-036-5

Query Match 58.1%; Score 30.2; DB 4; Length 50;  
Best Local Similarity 91.4%; Pred. No. 0.00052;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AATTATAGCACTACTATAGGAGCGGCGGCGC 35  
Db 3 AATTATAGCACTACTATAGGAGCGGCTGCC 37

RESULT 9  
US-09-944-036-37  
Sequence 37, Application US/09944036  
Patent No. 6582920  
GENERAL INFORMATION:  
APPLICANT: YANG, Yeasing Y.  
APPLICANT: BABOLA, Odile  
APPLICANT: TRAN, Nathalie  
APPLICANT: VERNET, Guy  
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
FILE REFERENCE: GP114-02 UT  
CURRENT APPLICATION NUMBER: US/09/944,036  
CURRENT FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/229,790  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 37  
LENGTH: 53  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: Oligonucleotide primer for Protease target  
NAME/KEY: promoter  
LOCATION: (1)..(33)  
US-09-944-036-37

Query Match 58.1%; Score 30.2; DB 4; Length 53;  
Best Local Similarity 74.5%; Pred. No. 0.00052;  
Matches 38; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 AATTATAGCACTACTATAGGAGCGGCGGCAACTGCTGGAATT 51  
Db 2 AAATTATAGCACTACTATAGGAGCAACAGCCATTCCTGCTTT 52

RESULT 10  
US-09-040-220D-7  
Sequence 7, Application US/09040220D  
Patent No. 6391311  
GENERAL INFORMATION:  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Kuo, Sophia S.  
TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR

;; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC  
;; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,  
;; FILE REFERENCE: P1122  
;; CURRENT APPLICATION NUMBER: US/09/040,220D  
;; CURRENT FILING DATE: 1998-03-17  
;; NUMBER OF SEQ ID NOS: 8  
;; SEQ ID NO 7  
;; LENGTH: 48  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; NAME/KEY: Artificial  
;; LOCATION: 1-48  
;; OTHER INFORMATION: Sequence is synthesized  
;; Patent No. 6391311  
US-09-040-220D-7

Query Match 57.3%; Score 29.8; DB 4; Length 48;  
Best Local Similarity 82.9%; Pred. No. 0.00076;  
Matches 34; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGCGGCGCCCAACTG 41  
Db 3 ATTCTATACGACTCACTATAGGCGCGCGAATCCAACTG 43

RESULT 11  
US-09-265-686-7  
;; Sequence 7, Application US/09265686  
;; Patent No. 6455283  
;; GENERAL INFORMATION:  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Kuo, Sophia S.  
;; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1  
;; FILE REFERENCE: P1122P2  
;; CURRENT APPLICATION NUMBER: US/09/265,686  
;; PRIOR FILING DATE: 1999-03-10  
;; PRIOR APPLICATION NUMBER: US 09/040,220  
;; PRIOR FILING DATE: 1998-03-17  
;; PRIOR APPLICATION NUMBER: US 09/184,216  
;; NUMBER OF SEQ ID NOS: 8  
;; SEQ ID NO 7  
;; LENGTH: 48  
;; TYPE: DNA  
;; ORGANISM: Artificial  
;; FEATURE:  
;; NAME/KEY: Artificial  
;; LOCATION: 1-48  
;; OTHER INFORMATION: Sequence is synthesized  
;; Patent No. 6455283  
US-09-265-686-7

Query Match 57.3%; Score 29.8; DB 4; Length 48;  
Best Local Similarity 82.9%; Pred. No. 0.00076;  
Matches 34; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGCGGCGCCCAACTG 41  
Db 3 ATTCTATACGACTCACTATAGGCGCGCGAATCCAACTG 43

RESULT 12  
US-09-723-749-7  
;; Sequence 7, Application US/09723749  
;; Patent No. 6620784  
;; GENERAL INFORMATION:  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Kuo, Sophia S.  
;; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1  
;; FILE REFERENCE: P1122P2D1  
;; CURRENT APPLICATION NUMBER: US/09/723,749

;; CURRENT FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: US 09/265,686  
;; PRIOR FILING DATE: 1999-03-10  
;; PRIOR APPLICATION NUMBER: US 09/040,220  
;; PRIOR FILING DATE: 1998-03-17  
;; PRIOR APPLICATION NUMBER: US 09/184,216  
;; NUMBER OF SEQ ID NOS: 8  
;; SEQ ID NO 7  
;; LENGTH: 48  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; NAME/KEY: Artificial  
;; LOCATION: 1-48  
;; OTHER INFORMATION: Sequence is synthesized  
;; Patent No. 6620784  
US-09-723-749-7

Query Match 57.3%; Score 29.8; DB 4; Length 48;  
Best Local Similarity 82.9%; Pred. No. 0.00076;  
Matches 34; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGCGGCGCCCAACTG 41  
Db 3 ATTCTATACGACTCACTATAGGCGCGCGAATCCAACTG 43

RESULT 13  
US-08-162-836-10  
;; Sequence 10, Application US/08162836  
;; Patent No. 5554516  
;; GENERAL INFORMATION:  
;; APPLICANT: Daniel L. Kacian  
;; APPLICANT: Diane L. McAllister  
;; APPLICANT: Sherrol H. McDonough  
;; APPLICANT: Nani Bhushan Dattagupta  
;; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AMPLIFICATION  
;; NUMBER OF SEQUENCES: 17  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 611 West Sixth Street  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 90017  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
;; COMPUTER: IBM compatible  
;; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
;; SOFTWARE: Wordperfect (Version 5.1)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/162,836  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/879,686  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Walburg, Richard J.  
;; REGISTRATION NUMBER: 32,327  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 47  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear

US-08-162-836-10

Query Match 56.9%; Score 29.6; DB 1; Length 47;  
Best Local Similarity 79.5%; Pred. No. 0.00092;  
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCACTATAGGAGACGGGCGCCAACTGCTA 44  
1 AATTATACGACTCACTATAGGAGACGGGCGCCAACTGCTA 44

Db 1 AATTATACGACTCACTATAGGAGACGGGCGCCAACTGCTA 44

RESULT 14

US-08-345-861-6  
; Sequence 6, Application US/08345861  
; Patent No. 5766849  
; GENERAL INFORMATION:  
; APPLICANT: Sherrol H. McDonough  
; APPLICANT: Daniel L. Kacian  
; APPLICANT: Nanibushan Dattagupta  
; APPLICANT: Diane L. McAllister  
; APPLICANT: Philip Hammond  
; APPLICANT: Thomas B. Ryder  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AMPLIFICATION  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/345,861  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/925,405  
; FILING DATE: August 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Watburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 197/136  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 552-8400  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 47  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-345-861-6

Query Match 56.9%; Score 29.6; DB 1; Length 47;  
Best Local Similarity 79.5%; Pred. No. 0.00092;  
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCACTATAGGAGACGGGCGCCAACTGCTA 44  
1 AATTATACGACTCACTATAGGAGACGGGCGCCAACTGCTA 44

Db 1 AATTATACGACTCACTATAGGAGACGGGCGCCAACTGCTA 44

RESULT 15

US-08-479-105A-6  
; Sequence 6, Application US/08479105A  
; Patent No. 5908744  
; GENERAL INFORMATION:

APPLICANT: Diane L. McAllister  
APPLICANT: Philip Hammond  
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE  
TITLE OF INVENTION: AMPLIFICATION  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: MS DOS (5.0)  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/479,105A  
; FILING DATE: June 6, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/345,861  
; FILING DATE: No. 5908744ember 28, 1994  
; APPLICATION NUMBER: 07/925,405  
; FILING DATE: August 4, 1992  
; APPLICATION NUMBER: 07/855,732  
; FILING DATE: March 19, 1992  
; APPLICATION NUMBER: 07/550,837  
; FILING DATE: July 10, 1990  
; APPLICATION NUMBER: 07/379,501  
; FILING DATE: July 11, 1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heber, Sheldon O.  
; REGISTRATION NUMBER: 38,179  
; REFERENCE/DOCKET NUMBER: 213/067  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 47 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-479-105A-6

Query Match 56.9%; Score 29.6; DB 2; Length 47;  
Best Local Similarity 79.5%; Pred. No. 0.00092;  
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCACTATAGGAGACGGGCGCCAACTGCTA 44  
1 AATTATACGACTCACTATAGGAGACGGGCGCCAACTGCTA 44

Db 1 AATTATACGACTCACTATAGGAGACGGGCGCCAACTGCTA 44

Search completed: August 31, 2004, 04:43:18  
Job time : 82.7143 secs

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GenCore version 5.1.6.  
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OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 01:37:23 ; Search time 3789.92 Seconds  
(without alignments)  
67.525 Million cell updates/sec

Title: US-10-001-407-15

Perfect score: 52

Sequence: 1 aattatatacgaactcactat.....gccaaactgtctaggatttc 52

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3337270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 2018620

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

Published Applications NA:\*

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11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	52	14	US-10-001-407-15
2	36.4	70.0	50	13	US-10-461-790-100
3	36.4	70.0	50	13	US-10-632-658-8
4	36.4	70.0	50	14	US-10-001-407-17
5	36.4	70.0	51	13	US-10-632-658-26
6	36	69.2	54	15	US-10-244-490-2
7	31.8	61.2	52	9	US-09-944-036-7
8	31.8	61.2	52	16	US-10-425-975-7
9	31.4	60.4	49	15	US-10-273-707-38
10	30.4	58.5	52	15	US-10-244-490-15
11	30.2	58.1	50	9	US-09-944-036-5
12	30.2	58.1	50	16	US-10-425-975-5
13	30.2	58.1	53	9	US-09-944-036-37
14	30.2	58.1	53	16	US-10-425-975-37

15	29.8	57.3	48	15	US-10-178-442-7	Sequence 7, Appl1
16	29.6	56.9	52	13	US-10-231-843-9	Sequence 9, Appl1
17	29.6	56.9	53	13	US-10-461-790-36	Sequence 36, Appl1
18	29.4	56.5	45	13	US-10-461-790-48	Sequence 48, Appl1
19	29.4	56.5	47	13	US-10-461-790-39	Sequence 39, Appl1
20	29.2	56.2	45	15	US-10-244-490-39	Sequence 39, Appl1
21	29.2	56.2	47	15	US-10-245-988-2	Sequence 2, Appl1
22	29	55.8	55	13	US-10-461-790-116	Sequence 116, Appl1
23	28.8	55.4	48	13	US-10-632-658-24	Sequence 24, Appl1
24	28.8	55.4	49	13	US-10-632-658-28	Sequence 28, Appl1
25	28.8	55.4	50	9	US-09-944-036-8	Sequence 8, Appl1
26	28.8	55.4	50	16	US-10-425-975-8	Sequence 8, Appl1
27	28.6	55.0	54	13	US-10-461-790-38	Sequence 38, Appl1
28	28.4	54.6	39	15	US-10-077-383-25	Sequence 25, Appl1
29	28.4	54.6	45	13	US-10-461-790-49	Sequence 49, Appl1
30	28.4	54.6	51	13	US-10-363-852-2	Sequence 2, Appl1
31	28.4	54.6	53	15	US-10-231-843-5	Sequence 5, Appl1
32	28.4	54.6	57	14	US-10-001-407-18	Sequence 18, Appl1
33	28.4	54.6	61	15	US-10-077-383-18	Sequence 18, Appl1
34	28.2	54.2	48	14	US-10-006-009-42	Sequence 42, Appl1
35	28.2	54.2	51	15	US-10-244-490-25	Sequence 25, Appl1
36	28.2	54.2	53	15	US-10-231-843-3	Sequence 3, Appl1
37	28.2	54.2	55	15	US-10-231-843-25	Sequence 25, Appl1
38	28.2	54.2	56	15	US-10-231-843-7	Sequence 7, Appl1
39	28	53.8	32	9	US-09-944-036-3	Sequence 3, Appl1
40	28	53.8	32	16	US-10-425-975-3	Sequence 3, Appl1
41	28	53.8	35	9	US-09-202-972-16	Sequence 16, Appl1
42	28	53.8	45	13	US-10-461-790-47	Sequence 47, Appl1
43	28	53.8	48	9	US-09-975-408-7	Sequence 7, Appl1
44	28	53.8	48	14	US-10-075-579-7	Sequence 7, Appl1
45	28	53.8	49	15	US-10-244-490-5	Sequence 5, Appl1

#### ALIGNMENTS

RESULT 1

US-10-001-407-15

Sequence 15, Application US/10001407

Publication No. US20020177127A1

GENERAL INFORMATION:

APPLICANT: Yang, Yeasing

APPLICANT: Burrell, Terrie

TITLE OR INVENTION: Compositions and Methods for Detecting

TITLE OR INVENTION: Human Immunodeficiency Virus 2 (HIV-2)

FILE REFERENCE: GP117-03.UT

CURRENT APPLICATION NUMBER: US/10/001.407

CURRENT FILING DATE: 2001-10-22

PRIOR APPLICATION NUMBER: 60/242,620

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/280,058

PRIOR FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 15

LENGTH: 52

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: T7 promoter primer having a promoter sequence

OTHER INFORMATION: appended at the 5' end of an HIV-2 complementary

OTHER INFORMATION: primer sequence

US-10-001-407-15

Query Match 100.0%; Score 52; DB 14; Length 52;  
Best Local Similarity 100.0%; Pred. No. 5.5e-13;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATTATATACGACTCTATATAGGAGACGGCGCAACCTGCTGGGATTTT 52

Db 1 AATTATATACGACTCTATATAGGAGACGGCGCAACCTGCTGGGATTTT 52

```
RESULT 2
US-10-461-790-100
; Sequence 100, Application US/10461790
; Publication No. US20040029111A1
; GENERAL INFORMATION:
; APPLICANT: Linmen, Jeffery M.
; APPLICANT: Kolk, Daniel P.
; APPLICANT: Dockter, Janel M.
; APPLICANT: Getman, Damon K.
; APPLICANT: Yoshimura, Tadashi
; APPLICANT: Ho-Sing-Ioy, Marcy
; APPLICANT: Stringfellow, Leslie A.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: Hepatitis B Virus
; FILE REFERENCE: GP134-02.UT
; CURRENT APPLICATION NUMBER: US/10/461,790
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/389,393
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-specific promoter-primer
US-10-461-790-100
```

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Query Match          70.0%; Score 36.4; DB 13; Length 50;
Best Local Similarity 94.2%; Pred. No. 4.7e-06;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
```

```
QY 1 AATTTAATGAGCTACTATAGGAGACGGCGCCCAACTGCTAGGATTTT 52
Db 1 AATTTAATGAGCTACTATAGGAGACGGCGCCCA--CTGCTAGGATTTT 50
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```
RESULT 3
US-10-632-658-8
; Sequence 8, Application US/10632658
; Publication No. US20040053223A1
; GENERAL INFORMATION:
; APPLICANT: Bee, Gary G.
; APPLICANT: Yang, Yeasing Y.
; APPLICANT: Kolk, Dan
; APPLICANT: Giachetti, Cristina
; APPLICANT: McDonough, Sherrol H.
; TITLE OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
; FILE REFERENCE: GP103-02.UT
; CURRENT APPLICATION NUMBER: US/10/632,658
; PRIOR FILING DATE: 2003-08-01
; TITLE OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
; FILE REFERENCE: GP103-02.UT
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/143,072
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amplification oligomer with 5' promoter sequence,
US-10-632-658-8
```

```
Query Match          70.0%; Score 36.4; DB 13; Length 50;
Best Local Similarity 94.2%; Pred. No. 4.7e-06;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
```

```
Db 1 AATTTAATGAGCTACTATAGGAGACGGCGCCCA--CTGCTAGGATTTT 50
```

```
RESULT 4
US-10-001-407-17
; Sequence 17, Application US/10001407
; Publication No. US20020177127A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Yeasing
; APPLICANT: Butrell, Terrie
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
; FILE REFERENCE: GP117-03.UT
; CURRENT APPLICATION NUMBER: US/10/001,407
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T7 promoter primer having a promoter sequence
; OTHER INFORMATION: appended at the 5' end of the sequence given as
US-10-001-407-17
```

```
Query Match          70.0%; Score 36.4; DB 14; Length 50;
Best Local Similarity 94.2%; Pred. No. 4.7e-06;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
```

```
QY 1 AATTTAATGAGCTACTATAGGAGACGGCGCCCAACTGCTAGGATTTT 52
Db 1 AATTTAATGAGCTACTATAGGAGACGGCGCCCA--CTGCTAGGATTTT 50
```

```
RESULT 5
US-10-632-658-26
; Sequence 26, Application US/10632658
; Publication No. US20040053223A1
; GENERAL INFORMATION:
; APPLICANT: Bee, Gary G.
; APPLICANT: Yang, Yeasing Y.
; APPLICANT: Kolk, Dan
; APPLICANT: Giachetti, Cristina
; APPLICANT: McDonough, Sherrol H.
; TITLE OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
; FILE REFERENCE: GP103-02.UT
; CURRENT APPLICATION NUMBER: US/10/632,658
; PRIOR FILING DATE: 2003-08-01
; TITLE OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
; FILE REFERENCE: GP103-02.UT
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/143,072
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amplification oligomer with 5' promoter sequence,
US-10-632-658-26
```

```
Query Match          70.0%; Score 36.4; DB 13; Length 51;
Best Local Similarity 94.2%; Pred. No. 4.7e-06;
```



Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy 1 AATTATACGACTCTATATAGGAGACGGCGCCCAACTGCTAGGATTTT 52  
Db 1 AATTATACGACTCTATATAGGAGACGGCGCCA--CTGCTAGGATTTT 50

## RESULT 6

US-10-244-490-2  
; Sequence 2, Application US/10244490  
; Publication No. US20030152916A1  
; GENERAL INFORMATION:  
; APPLICANT: KACIAN, DANIEL L.  
; APPLICANT: FULTZ, TIMOTHY J.  
; APPLICANT: MCDONOUGH, SHERROL H.  
; TITLE OF INVENTION: DETECTION OF HIV  
; FILE REFERENCE: 218/130  
; CURRENT APPLICATION NUMBER: US/10/244,490  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US/09/168,947  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 08/469,067  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: 07/550,837  
; PRIOR FILING DATE: 1990-07-10  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 54  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized nucleic acid molecule  
; US-10-244-490-2

Query Match 69.2%; Score 36; DB 15; Length 54;  
Best Local Similarity 80.8%; Pred. No. 7.2e-06;  
Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCTATATAGGAGACGGCGCCCAACTGCTAGGATTTT 52  
Db 1 AATTATACGACTCTATATAGGAGACGAGCACTTCCCTGCGGACTTT 52

## RESULT 7

US-09-944-036-7  
; Sequence 7, Application US/09944036  
; Patent No. US20020055095A1  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP14-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Protease target  
; NAME/KEY: promoter  
; LOCATION: (1)..(32)

US-09-944-036-7

Query Match 61.2%; Score 31.8; DB 9; Length 52;  
Best Local Similarity 76.5%; Pred. No. 0.00053;  
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCTATATAGGAGACGGCGCCCAACTGCTAGGATTTT 51  
Db 1 AATTATACGACTCTATATAGGAGACGACGACATCCATTCCTGACTTT 51

## RESULT 8

US-10-425-975-7  
; Sequence 7, Application US/10425975  
; Publication No. US20030228574A1  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP14-02.UT  
; CURRENT APPLICATION NUMBER: US/10/425,975  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US/09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Protease target  
; NAME/KEY: promoter  
; LOCATION: (1)..(32)  
; US-10-425-975-7

Query Match 61.2%; Score 31.8; DB 16; Length 52;  
Best Local Similarity 76.5%; Pred. No. 0.00053;  
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCTATATAGGAGACGGCGCCCAACTGCTAGGATTTT 51  
Db 1 AATTATACGACTCTATATAGGAGACGACGACATCCATTCCTGACTTT 51

## RESULT 9

US-10-273-707-38  
; Sequence 38, Application US/10273707  
; Publication No. US2003010448A1  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, J.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; FILE REFERENCE: GP097-03.DV1  
; CURRENT APPLICATION NUMBER: US/10/273,707  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 09/493,491  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38

LENGTH: 49  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
FEATURE:  
NAME/KEY: Promoter  
LOCATION: (1) .. (28)  
US-10-273-707-38

Query Match  
Best Local Similarity 60.4%; Score 31.4; DB 15; Length 49;  
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGCGGCGCCCAACTG 41  
DB 2 AATTATACGACTCACTATAGGAGCGGCGCTGCTGCTG 42

RESULT 10  
US-10-244-490-15  
Sequence 15, Application US/10244490  
Publication No. US20030152916A1  
GENERAL INFORMATION:  
APPLICANT: KACIAN, DANIEL L.  
APPLICANT: PUTZ, TIMOTHY J.  
TITLE OF INVENTION: DETECTION OF HIV  
FILE REFERENCE: 218/130  
CURRENT APPLICATION NUMBER: US/10/244,490  
PRIOR FILING DATE: 2002-09-16  
PRIOR APPLICATION NUMBER: US/09/168,947  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 08/469,067  
PRIOR FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: 07/550,837  
PRIOR FILING DATE: 1990-07-10  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 52  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized nucleic acid molecule  
US-10-244-490-15

Query Match  
Best Local Similarity 58.5%; Score 30.4; DB 15; Length 52;  
Matches 34; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGCGGCGCCCAACT 40  
DB 1 AATTATACGACTCACTATAGGAGCGGCGCTGCTCTT 40

RESULT 11  
US-09-944-036-5  
Sequence 5, Application US/09944036  
Patent No. US20020055095A1  
GENERAL INFORMATION:  
APPLICANT: YANG, Yeasing Y.  
APPLICANT: BRENTANO, Steven T.  
APPLICANT: BABOLA, Odile  
APPLICANT: TRAN, Nathalie  
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
FILE REFERENCE: GP114-02.UT  
CURRENT APPLICATION NUMBER: US/09/944,036  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/229,790

PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 5  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
NAME/KEY: Promoter  
LOCATION: (1) .. (29)  
US-09-944-036-5

Query Match  
Best Local Similarity 58.1%; Score 30.2; DB 9; Length 50;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGCGGCGCC 35  
DB 3 AATTATACGACTCACTATAGGAGAGTGGCTCC 37

RESULT 12  
US-10-425-975-5  
Sequence 5, Application US/10425975  
Publication No. US20030228574A1  
GENERAL INFORMATION:  
APPLICANT: YANG, Yeasing Y.  
APPLICANT: BRENTANO, Steven T.  
APPLICANT: BABOLA, Odile  
APPLICANT: TRAN, Nathalie  
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
FILE REFERENCE: GP114-02.UT  
CURRENT APPLICATION NUMBER: US/10/425,975  
CURRENT FILING DATE: 2003-04-28  
PRIOR APPLICATION NUMBER: US/09/944,036  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/229,790  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 5  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
NAME/KEY: Promoter  
LOCATION: (1) .. (29)  
US-10-425-975-5

Query Match  
Best Local Similarity 58.1%; Score 30.2; DB 16; Length 50;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGCGGCGCC 35  
DB 3 AATTATACGACTCACTATAGGAGAGTGGCTCC 37

RESULT 13  
US-09-944-036-37  
Sequence 37, Application US/09944036  
Patent No. US20020055095A1  
GENERAL INFORMATION:  
APPLICANT: YANG, Yeasing Y.  
APPLICANT: BRENTANO, Steven T.  
APPLICANT: BABOLA, Odile

APPLICANT: TRAN, Nathalie  
APPLICANT: VERNET, Guy  
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS  
FILE REFERENCE: GP14-02.UT  
CURRENT APPLICATION NUMBER: US/09/944,036  
CURRENT FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/229,790  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 37  
LENGTH: 53  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: Oligonucleotide primer for Protease target  
NAME/KEY: Promoter  
LOCATION: (1)..(33)  
US-09-944-036-37

Query Match 58.1%; Score 30.2; DB 9; Length 53;  
Best Local Similarity 74.5%; Pred. No. 0.0027;  
Matches 38; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 AATTAAATACGACTACTATATAGGAGACGGGCGCAACTGCTAGGATTT 51  
DB 2 AAATTATACGACTACTATATAGGAGACACAGCCATCTCTGCTTT 52

RESULT 14  
US-10-425-975-37  
Sequence 37, Application US/10425975  
Publication No. US20030228574A1  
GENERAL INFORMATION:  
APPLICANT: YANG, Yeasing Y.  
APPLICANT: BRENTANO, Steven T.  
APPLICANT: BABOLA, Odile  
APPLICANT: TRAN, Nathalie  
APPLICANT: VERNET, Guy  
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS  
FILE REFERENCE: GP14-02.UT  
CURRENT APPLICATION NUMBER: US/10/425,975  
CURRENT FILING DATE: 2003-04-28  
PRIOR APPLICATION NUMBER: US/09/944,036  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/229,790  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 37  
LENGTH: 53  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: Oligonucleotide primer for Protease target  
OTHER INFORMATION: sequence  
FEATURE:  
NAME/KEY: Promoter  
LOCATION: (1)..(33)  
US-10-425-975-37

Query Match 58.1%; Score 30.2; DB 16; Length 53;  
Best Local Similarity 74.5%; Pred. No. 0.0027;  
Matches 38; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 AATTAAATACGACTACTATATAGGAGACGGGCGCAACTGCTAGGATTT 51  
DB 2 AAATTATACGACTACTATATAGGAGACACAGCCATCTCTGCTTT 52

RESULT 15  
US-10-178-442-7  
Sequence 7, Application US/10178442  
Publication No. US20030113870A1  
GENERAL INFORMATION:  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Kuo, Sophia S.  
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1  
FILE REFERENCE: 11669.112USD2  
CURRENT APPLICATION NUMBER: US/10/178,442  
CURRENT FILING DATE: 2002-09-24  
PRIOR APPLICATION NUMBER: US 09/265,686  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: US 09/184,216  
PRIOR FILING DATE: 1998-11-02  
PRIOR APPLICATION NUMBER: US 09/040,220  
PRIOR FILING DATE: 1998-03-17  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7  
LENGTH: 48  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Sequence is synthesized  
US-10-178-442-7

Query Match 57.3%; Score 29.8; DB 15; Length 48;  
Best Local Similarity 82.9%; Pred. No. 0.004;  
Matches 34; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AATTAAATACGACTACTATATAGGAGACGGGCGCAACTG 41  
DB 3 ATTCTAATACGACTACTATATAGGAGCGGCGGAATCCAACCTG 43

Search completed: August 31, 2004, 06:17.10  
Job time : 3797.92 secs

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